

November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions .rnpbm (Published\_Applications\_NA\_Main) and .rnpbn (Published\_Applications\_NA\_New). Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions .rapbm (Published\_Applications\_AA\_Main) and .rapbn (Published\_Applications\_AA\_New).

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16	71.5	3.9	353	1	US-10-793-626-2040
7	71.5	3.9	565	1	US-10-485-713-300
8	71.5	3.9	249	7	US-11-054-515-1321
9	71.5	3.9	334	1	US-10-858-730-121
0	71.5	3.9	579	1	US-10-526-673-2
1	71.5	3.9	71	1	US-10-793-626-2832
2	71	3.9	584	7	US-11-108-864-19
3	71	3.9	934	7	US-10-821-234-1076
4	70.5	3.9	3717	1	US-10-858-730-2117
5	70.5	3.9	368	1	US-10-858-730-2117
6	70.5	3.9	609	7	US-11-058-555-2
7	70.5	3.9	645	1	US-10-510-386-32
8	70.5	3.9	1126	1	US-10-485-517-24
9	70	3.8	174	1	US-10-984-376-7
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1	69.5	3.8	239	1	US-10-485-517-24
2	69.5	3.8	457	7	US-11-074-176-12
3	69.5	3.8	635	7	US-11-113-837-16
4	69.5	3.8	1207	1	US-10-821-234-1109
5	69	3.8	423	7	US-11-082-389-1128
6	69	3.8	579	1	US-10-821-234-1352

ALIGNMENTS

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries									
; Sequence 227, Application US/10858730									
; Publication No. US2005055568A1									
; GENERAL INFORMATION:									
; APPLICANT: Bailey, Richard B.									
; APPLICANT: Blomquist, Paul									
; APPLICANT: Doten, Reed									
; APPLICANT: Driggers, Edward M.									
; APPLICANT: Madden, Kevin T.									
; APPLICANT: O'Leary, Jessica									
; APPLICANT: O'Toole, George									
; APPLICANT: Trueheart, Joshua									
; APPLICANT: Walbridge, Michael J.									
; APPLICANT: Yorgay, Peter S.									
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID									
; TITLE OF INVENTION: PRODUCTION									
; FILE REFERENCE: 14184-030001									
; CURRENT APPLICATION NUMBER: US/10/858,730									
; CURRENT FILING DATE: 2004-06-01									
; PRIORITY NUMBER: US 60/475,000									
; PRIORITY FILING DATE: 2003-05-30									
; PRIORITY APPLICATION NUMBER: US 60/551,860									
; PRIORITY FILING DATE: 2004-03-10									
; NUMBER OF SEQ ID NOS: 364									
; SOFTWARE: FastSEQ for Windows Version 4.0									
; SEQ ID NO: 227									
; LENGTH: 417									
; TYPE: PRT									
; ORGANISM: Escherichia coli									
; US-10-858-730-227									
SUMMARIES									
Result No.	Score		Query Match Length		ID	Description			
1	94	5.2	417	1	US-10-858-730-227	Sequence 227, App			
2	93.5	5.1	229	1	US-10-510-286-228	Sequence 228, App			
3	93	5.1	410	1	US-10-793-326-3258	Sequence 3258, App			
4	93	5.1	477	1	US-10-793-326-3250	Sequence 3250, App			
5	84	4.6	1992	7	US-11-013-759-3	Sequence 3, Appl			
6	84	4.6	1992	7	US-11-013-759-13	Sequence 13, Appl			
7	84	4.6	2047	7	US-11-013-759-4	Sequence 4, Appl			
8	84	4.6	2047	7	US-11-013-759-7	Sequence 7, Appl			
9	84	4.6	2053	7	US-11-013-759-9	Sequence 9, Appl			
10	83.5	4.6	585	1	US-10-510-286-20	Sequence 20, Appl			
11	83.5	4.6	594	1	US-10-510-286-38	Sequence 38, Appl			
12	83.5	4.6	721	7	US-11-060-320-5	Sequence 5, Appl			
13	81.5	4.5	543	1	US-10-495-664-3	Sequence 3, Appl			
14	81	4.4	348	1	US-10-793-626-2866	Sequence 2866, App			
15	79	4.3	334	1	US-10-802-389-728	Sequence 728, App			
16	79	4.3	444	7	US-11-074-176-170	Sequence 170, App			
17	78	4.3	259	1	US-10-510-386-108	Sequence 108, App			
18	76.5	4.2	251	7	US-11-054-151-1833	Sequence 1833, App			
19	75	4.1	249	7	US-11-054-151-1753	Sequence 1753, App			
20	75	4.1	524	7	US-11-082-389-10	Sequence 10, Appl			
21	73	4.0	1213	7	US-11-074-176-256	Sequence 256, App			
22	72.5	4.0	643	1	US-10-510-386-8	Sequence 8, Appl			
23	72	3.9	227	1	US-10-558-730-86	Sequence 86, Appl			
24	72	3.9	835	1	US-10-501-339-4	Sequence 4, Appl			
25	71.5	3.9	80	1	US-10-821-334-949	Sequence 949, Appl			
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Qy 230 PEGQQAL----DOLYQISN-----MDPKDGSAAVVLGYDRIGSEAYNOOLSE 273  
 Db 234 PRGULLAKGGSEELVYKSVAPPGQQGSPLNHVIASKAVAKAEAMEPFRKYQQVA- 292

Qy 274 KRAQSVDLVALVAKSIIPAGKISARGMGE-----SNPTGNTCDNYKARA 316  
 Db 293 KNAKAMVEFLERGY---KVSGSTTDNHFLFLVLDRKNTLGKEADAALGRA 340

**RESULT 2**

US-10-510-386-228  
 ; Sequence 228, Application US/10510386  
 ; Publication No. US20050244922A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Andersen, Jens Tonne  
 ; APPLICANT: Clausen, Ib Groth  
 ; APPLICANT: Jorgensen, Steen Troels  
 ; APPLICANT: Olesen, Peter Bjarke  
 ; APPLICANT: Rasmussen, Michael Dolberg  
 ; TITLE OF INVENTION: Improved Bacillus Host Cell  
 ; FILE REFERENCE: 10294/2004-US  
 ; CURRENT APPLICATION NUMBER: US/10/510,386  
 ; NUMBER OF SEQ ID NOS: 248  
 ; SOFTWARE: Patentin version 3.3  
 ; SEQ ID NO: 228  
 ; LENGTH: 229  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus licheniformis  
 US-10-510-386-228

Query Match Score 5.1%; Best Local Similarity 26.8%; Pred. No. 0.092; Length 229;  
 Matches 33; Conservative 22; Mismatches 51; Indels 17; Gaps 4;

Qy 215 LKSDVLFNFNKATLKPECGQOALDOLYQTLNSMDPKDGSAAVVLGYDRIGSEY---NQ 270  
 Db 116 LQEAVLFDGSKADLKDQAHPLHKIAVNLKSV---SNPIRVEGHSTDSPRISTYRFPSNWE 172

Qy 271 LSEKRAQSYVDLYVAK-GIPAGKITSARGMGESENPTGNTCDNYKARALIDCLAPDRRE 329  
 Db 173 LSARASTVIGYFTSKEKLDSSRFLAIGYADTKPVRDNRTES-----HMKENRRE 223

Qy 330 IEV 332  
 Db 224 IVI 226

**RESULT 3**  
 US-10-793-626-3258  
 ; Sequence 3258, Application US/10793626  
 ; Publication No. US20050255478A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIMMERLY, WILLIAM JOHN  
 ; TITLE OF INVENTION: STAPHYLOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
 ; FILE REFERENCE: PUS4800S  
 ; CURRENT APPLICATION NUMBER: US/10/793, 626  
 ; CURRENT FILING DATE: 2004-03-04  
 ; PRIOR FILING DATE: 1999-11-09  
 ; NUMBER OF SEQ ID NOS: 4472  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO: 3258  
 ; LENGTH: 410  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: amino acid sequence  
 US-10-793-626-3258

Query Match Score 5.1%; Best Local Similarity 20.1%; Pred. No. 0.27; Length 477;  
 Matches 74; Conservative 48; Mismatches 116; Indels 124; Gaps 20;

Qy 12 KDNTWYAGGLKGQHSDYHTGFYGNQFQNNNGPTRNDGAGAFGGQVNPNYLGFGEM--- 68  
 Db 75 KDNNGKNTYLIK-AQGKTEFYKNNSNTLG-----YNGNLLGPTKLKCGDKV 122

Qy 69 -----YDWLGRMAYKGSYDNG-----AFKAQGVQLTAKGY---- 99  
 Db 123 KIKLINNLDENTTEFHWHG-LEVNGKDGPSQVIKGKEKTIKFENQDSATLWYHPHS 181

Qy 100 PITDDDIYTRIGGMWYRADS-KGNVASTGYSRSEHDGTGUSPVFAGGVEAWTRD---IA 155  
 Db 182 PNTAK-QVYNGSLGLYIEDKKNNPP-----SDGKNDLPI-----IQDKTFVFS 226

Qy 156 TRLEYQVNNTGDAIGTVG-TRDNGHLSLGYSYRFQEDAAPVVAAPAPAPEVATKHF 214  
 Db 227 KKLNYSKTKD--EDGTQGDTLVNGIVN-----PKLTKEEK 261

Qy 156 TRLEYQVNNTGDAIGTVG-TRDNGHLSLGYSYRFQEDAAPVVAAPAPAPEVATKHF 214  
 Db 227 KKLNYSKTKD--EDGTQGDTLVNGIVN-----PKLTKEEK 261

Qy 215 LKSDVLF--FNFNKATLKPECGQOALDOLYQ---QLS-----NMPDRGDSAVLGYTDR 261  
 Db 262 IRLRLNGSNARDLNKLNSRNOSPEYIASDGCQLKNAKKLKEINLASSERKEIVIDISK 321

Qy 262 IGSE-----AYNQOLSEKRAQSYVDLYVAK-GIPAGKITSARGMGESENPTGNT 308  
 Db 322 KGBKISLVNDKTVLDPISNKEKSSNRGNTP--KVSK----KIKLEGMDNDNVTINGNK 373

Qy 309 CD 310  
 Db 374 FD 375

RESULT 4  
 US-10-793-626-3250  
 ; Sequence 3250, Application US/10793626  
 ; Publication No. US20050255478A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIMMERLY, WILLIAM JOHN  
 ; TITLE OF INVENTION: STAPHYLOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
 ; FILE REFERENCE: PUS4800S  
 ; CURRENT APPLICATION NUMBER: US/10/793, 626  
 ; CURRENT FILING DATE: 2004-03-04  
 ; PRIOR APPLICATION NUMBER: 60/164, 258  
 ; PRIOR FILING DATE: 1999-11-09  
 ; NUMBER OF SEQ ID NOS: 4472  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SBQ ID NO: 3250  
 ; LENGTH: 477  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: amino acid sequence  
 US-10-793-626-3250

Query Match Score 5.1%; Best Local Similarity 20.1%; Pred. No. 0.27; Length 477;  
 Matches 74; Conservative 48; Mismatches 116; Indels 124; Gaps 20;

Qy 12 KDNTWYAGGLKGQHSDYHTGFYGNQFQNNNGPTRNDGAGAFGGQVNPNYLGFGEM--- 68  
 Db 75 KDNNGKNTYLIK-AQGKTEFYKNNSNTLG-----YNGNLLGPTKLKCGDKV 122

Qy 69 -----YDWLGRMAYKGSYDNG-----AFKAQGVQLTAKGY---- 99  
 Db 123 KIKLINNLDENTTEFHWHG-LEVNGKDGPSQVIKGKEKTIKFENQDSATLWYHPHS 181

Qy 100 PITDDDIYTRIGGMWYRADS-KGNVASTGYSRSEHDGTGUSPVFAGGVEAWTRD---IA 155  
 Db 182 PNTAK-QVYNGSLGLYIEDKKNNPP-----SDGKNDLPI-----IQDKTFVFS 226

Qy 156 TRLEYQVNNTGDAIGTVG-TRDNGHLSLGYSYRFQEDAAPVVAAPAPAPEVATKHF 214  
 Db 227 KKLNYSKTKD--EDGTQGDTLVNGIVN-----PKLTKEEK 261

RESULT 5  
 US-11-013-759-3  
 Sequence 3, Application US/11013759  
 Publication No. US20050249747A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Loosmore, Sheena M.  
 ; APPLICANT: Sasaki, Ken  
 ; APPLICANT: Yang, Yan Ping  
 ; APPLICANT: Klein, Michel H.  
 ; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE  
 ; FILE REFERENCE: 1038-921MIS:jb  
 ; CURRENT APPLICATION NUMBER: US/11/013,759  
 ; CURRENT FILING DATE: 2004-12-16  
 ; PRIORITY APPLICATION NUMBER: US/09/361,619  
 ; PRIORITY FILING DATE: 1999-07-27  
 ; NUMBER OF SEQ ID NOS: 32  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 13  
 ; LENGTH: 1992  
 ; TYPE: PRT  
 ; ORGANISM: Moraxella catarrhalis  
 US-11-013-759-13

Query Match Score 4.6%; DB 7; Length 1992;  
 Best Local Similarity 20.1%; Pred. No. 11;  
 Matches 78; Conservative 47; Mismatches 142; Indels 122; Gaps 17;

Qy 18 AGGRGNSQYHDTGFGNGFQNNGPTRNDQAGA---FGGYQVNPNYLG---FEM 67  
 Db 959 SGLKAGKSTLNQGL---STKNPFGSEQTQVAGCVKFAKVNNNGVVGAGIDGTRI 1012  
 Qy 68 GYDWLGRMAYKGVDNG-----AFKAQGVQLT-AKLGYPITDDDIYTRIGGMWNR-- 117  
 Db 1013 TRDEIGFTGTNSLDKSKPHLSRDKGINAGKKITNQSGEIAQNSHDAVT--GGKLYDLK 1070  
 Qy 118 ATRELKYQVNNGDAGTGPTRDPNGMLSLGVSYRFGOEDAAPVVAAPAPAPEVATKHF 214  
 Db 1071 TELENKISSATAQNSLHEFSVADEQMNFTVSNPYSSYDT-----SKTSVD 1157  
 Qy 155 ATRELKYQVNNGDAGTGPTRDPNGMLSLGVSYRFGOEDAAPVVAAPAPAPEVATKHF 214  
 Db 1119 IT-----FAGENG-ITTKVNGKVVVRGIDOTKG-----LTTPKLTVNNN 1157  
 Qy 215 LKSDVLFNFNKATLKPGQDLYTOLSNNMDPKDGSAAVVLGYTDIGSEAYNQOLSEK 274  
 Db 1158 GK5IVDSQN-----GQNTTGLSNTLNQANTNDKGSVRVTEQGNITKDE-----DKT 1204  
 Qy 275 RAQSVDVYLAKGIPAGKISARGMGS-----NPVTGNTC-----DNVKARAA 317  
 Db 1205 RAASIVDVSA-----GPNLQNGEADEVFVSTYDTNFADEGNATTAKVTDTSKTSKV 1258  
 Qy 318 LIDCLAPDRRVIEVK--GYKEVVTQPG 344  
 Db 1259 VTDVNVDTTIEVKDKUGVKTTLSTG 1287

RESULT 7  
 US-11-013-759-4  
 Sequence 4, Application US/11013759  
 Publication No. US20050249747A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Loosmore, Sheena M.  
 ; APPLICANT: Sasaki, Ken  
 ; APPLICANT: Yang, Yan Ping  
 ; APPLICANT: Klein, Michel H.  
 ; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE  
 ; FILE REFERENCE: 1038-921MIS:jb  
 ; CURRENT APPLICATION NUMBER: US/11/013,759  
 ; CURRENT FILING DATE: 2004-12-16  
 ; PRIORITY APPLICATION NUMBER: US/09/361,619  
 ; PRIORITY FILING DATE: 1999-07-27  
 ; NUMBER OF SEQ ID NOS: 32  
 ; SOFTWARE: PatentIn Ver. 2.1

RESULT 6  
 US-11-013-759-13

; SEQ ID NO 4  
; LENGTH: 2047  
; TYPE: PRT  
; ORGANISM: Moraxella catarrhialis  
; US-11-013-759-4

Query Match Similarity 4.6%; Score 84; DB 7; Length 2047;  
Best Local Similarity 20.1%; Pred. No. 11; Mismatches 142; Indels 122; Gaps 17;  
Matches 78; Conservative 47; MisMatch 142; Del 122; Insert 122

Qy 18 AGGKLIGWSSYHDTCFYGNCFQNNNGPTNDOLGAGA---FEGYQVNPNYLG----FEM 67  
Db 1014 SGLKAGKSTLNDGGL-----SINKPNTSSEQIQVNGADGVKFAKVNNNGVVGAGIDGTR 1067

Qy 68 GYDMLGRMAYKGSVDNG-----AFKAQGVOLT-AKUGYPTDDDIYTRIGGMWFR- 117  
Db 1068 TRDEIGFTGTGNGSLDKSKPHLSRGKDNAGGKKITNNQSGEIAQNSHDAVT -GGKIYDLK 1124

Qy 118 -----ADSKGNAYSTGVRSRBDTCTSPVSPFAGGYEWAVTRDI 154  
Db 1126 TELENKISSTAKTAQNSLHEFSVADEQMNFTVSNPSSYDT-----SKTSVD 1173

Qy 155 ATRLYEQVNNGPTNDOLGAGA---FEGYQVNPNYLG----FEM 67  
Db 1174 IT-----FAGENG-ITTKVNGKVVVRGIDOTKG-----LTTPLTVGNNN 1212

Qy 215 LKSDVLFNFNKATLKPECGQALDOLYTOLSNNMDPKDGSAAVVLGYTRIGSEAYNQOLSEK 274  
Db 1213 GKGIVIDDSN-----GONTITGLSNTLANTNDKGSRVTRTEQGNNIKDE-----DKT 1259

Qy 275 RAQSVVDYLVAKGIPAKISARGMGS-----NPVTGNTC-----DNVKARA 317  
Db 1260 RAASIVDVLSA-----GFLNLQSGNEAVDFVSTYDTNFADESNATTAKVTDTSK 1313

Qy 318 LIDCLAPDRRVIEVK--GYKEVVTOPAG 344  
Db 1314 VYDVNVDDTTIEVKDKLKVKTTLSTG 1342

RESULT 9  
US-11-013-759-9  
Sequence 9; Application US/11013759  
Publication No. US2005024977A1  
GENERAL INFORMATION:  
APPLICANT: Loosmore, Sheena M.  
APPLICANT: Sasaki, Ken  
APPLICANT: Yang, Yan Ping  
APPLICANT: Klein, Michel H.  
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE  
TITLE OF INVENTION: PROTEIN OF MORAXELLA  
FILE REFERENCE: 1038-921MIS.jb  
CURRENT APPLICATION NUMBER: US/11/013,759  
CURRENT FILING DATE: 2004-12-16  
PRIOR APPLICATION NUMBER: US/09/361,519  
PRIOR FILING DATE: 1999-07-27  
NUMBER OF SEQ ID NOS: 32  
SEQ ID NO 9  
LENGTH: 2053  
TYPE: PRT  
ORGANISM: Moraxella catarrhalis  
US-11-013-759-9

Query Match 4.6%; Score 84; DB 7; Length 2053;  
Best Local Similarity 20.4%; Pred. No. 11; Mismatches 133; Indels 120; Gaps 17;  
Matches 76; Conservative 43; Mismatches 133; Indels 120; Gaps 17;

Qy 39 NNNG---PRNDQGAGARG---GYQVNPNYLG----FEMGYDWLGRMAYKGSVDNG 84  
Db 1034 NNNGLISKTASNEQIQVGAQSVKFAMVNGVAGIDGTRTRIBGFTGTNGSLDKS 1093

Qy 85 -----AFKAQGVQLDLDIYTRIGGMWFR-----117  
Db 1094 KPHLSRGKDNAGGKKITNNQSGEIAQNSHDAVT -GGKIYDLKTELENKISSTAKTQNS 1151

Qy 118 -----ADSKGNAYSTGVRSRBDTCTSPVSPFAGGYEWAVTRDIATRLEYQVNNGIAGT 171  
Db 1152 LRHFSVADEQMNFTVSNPSSYDT-----SKTSVD-----PAGENG- 1190

RESULT 8  
US-11-013-759-7  
Sequence 7; Application US/11013759  
Publication No. US2005024977A1  
GENERAL INFORMATION:  
APPLICANT: Sasaki, Ken  
APPLICANT: Yang, Yan Ping  
APPLICANT: Klein, Michel H.  
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE  
FILE REFERENCE: 1038-921MIS.jb  
CURRENT APPLICATION NUMBER: US/11/013,759  
CURRENT FILING DATE: 2004-12-16  
PRIOR APPLICATION NUMBER: US/09/361,619  
PRIOR FILING DATE: 1999-07-27  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 2047  
TYPE: PRT  
ORGANISM: Moraxella catarrhalis  
US-11-013-759-7

Query Match 4.6%; Score 84; DB 7; Length 2047;  
Best Local Similarity 20.1%; Pred. No. 11; Mismatches 142; Indels 122; Gaps 17;  
Matches 78; Conservative 47; MisMatch 142; Del 122; Insert 122

Qy 18 AGGKLIGWSSYHDTCFYGNCFQNNNGPTNDOLGAGA---FEGYQVNPNYLG----FEM 67  
Db 1014 SGLKAGKSTLNDGGL-----SINKPNTSSEQIQVNGADGVKFAKVNNNGVVGAGIDGTR 1067

Qy 68 GYDMLGRMAYKGSVDNG-----AFKAQGVOLT-AKUGYPTDDDIYTRIGGMWFR- 117

Db 1280 GFNLQGNGRAVDVFYSTDDTVNFANGNTTAKVYDDTSKTSKVYDVNVDTTIEVKDKK 1339  
 Qy 334 -GYKBVVTOPAG 344  
 Db 1340 LGVKTTLTSTG 1351

RESULT 10  
 US-10-510-386-20  
 Sequence 20, Application US/10510386  
 Publication No. US2005024922A1  
 GENERAL INFORMATION:  
 APPLICANT: Andersen, Jens Toerne  
 APPLICANT: Clausen, Ib Groth  
 APPLICANT: Jorgensen, Steen Troels  
 APPLICANT: Olsen, Peter Bjørke  
 APPLICANT: Rasmussen, Michael Dolberg  
 TITLE OF INVENTION: Improved Bacillus Host Cell  
 FILE REFERENCE: 10294.204-US  
 CURRENT APPLICATION NUMBER: US/10/510,386  
 CURRENT FILING DATE: 2004-10-04  
 NUMBER OF SEQ ID NOS: 28  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO 20  
 LENGTH: 585  
 TYPE: PRT  
 ORGANISM: *Bacillus licheniformis*  
 US-10-510-386-20

Query Match 4.6%; Score 83.5; DB 1; Length 585;  
 Best Local Similarity 26.1%; Pred. No. 2.4;  
 Matches 52; Conservative 20; Mismatches 70; Indels 57; Gaps 11;

Qy 98 GYITDDIIDIYTRGGMWRADSKGNATSGVSRSENDTGSPVFAVGVEAVTRDIATR 157  
 Db 382 GYVLDREGWGRL-NLFSAADGYAF -----TKNVTVTMDSAKGFFH--TAD--- 426  
 Qy 158 LEVQWNVNIGDAGTV-----GTRPDNGMLSGLGVSYRFGQDAA--PV 197  
 Db 427 ---RWRNDISGTRKLTKGGTGALEGNTYSGTRIDQGTLEGGSETAFGRGDVAINGG 483  
 Qy 198 VAPAP-----APEVATKHTFLKSVDLFNFNKATLKPEGOALDQLYTOLSN 245  
 Db 484 ILKEDAPGKLIIEGDKYROSAGKILELQLSKDKQLIKKGKARLK--GTURLN--FT--DN 537  
 Qy 246 MDPKDGSAVVLGTYDRIGS 264  
 Db 538 YVPADGSAIT-FRKHGS 555

RESULT 11  
 US-10-510-386-38  
 Sequence 3, Application US/10510386  
 Publication No. US2005024922A1  
 GENERAL INFORMATION:  
 APPLICANT: Andersen, Jens Toerne  
 APPLICANT: Clausen, Ib Groth  
 APPLICANT: Jorgensen, Steen Troels  
 APPLICANT: Olsen, Peter Bjørke  
 APPLICANT: Rasmussen, Michael Dolberg  
 TITLE OF INVENTION: Improved Bacillus Host Cell  
 FILE REFERENCE: 10294.204-US  
 CURRENT APPLICATION NUMBER: US/10/510,386  
 NUMBER OF SEQ ID NOS: 248  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO 38  
 LENGTH: 594  
 TYPE: PRT  
 ORGANISM: *Bacillus licheniformis*  
 US-10-510-386-38

Query Match 4.6%; Score 83.5; DB 1; Length 594;

Best Local Similarity 26.1%; Pred. No. 2.4;  
 Matches 52; Conservative 20; Mismatches 70; Indels 57; Gaps 11;  
 Qy 98 GYITDDIIDIYTRGGMWRADSKGNATSGVSRSENDTGSPVFAVGVEAVTRDIATR 157  
 Db 387 GYPVLDREGWGRL-NLFSAADGYAF -----TKNVTVTMDSAKGFFH--TAD--- 431  
 Qy 158 LEVQWNVNIGDAGTV-----GTRPDNGMLSGLGVSYRFGQDAA--PV 197  
 Db 432 ---RWRNDISGTRKLTKGGTGALEGNTYSGTRIDQGTLEGGSETAFGRGDVAINGG 488  
 Qy 198 VAPAP-----APEVATKHTFLKSVDLFNFNKATLKPEGOALDQLYTOLSN 245  
 Db 489 ILKEDAPGKLIIEGDKYROSAGKILELQLSKDKQLIKKGKARLK--GTURLN--FT--DN 542  
 Qy 246 MDPKDGSAVVLGTYDRIGS 264  
 Db 543 YVPADGSAIT-FRKHGS 560

RESULT 12  
 US-11-060-920-5  
 Sequence 5, Application US/11060920  
 Publication No. US20050244378A1  
 GENERAL INFORMATION:  
 APPLICANT: Kaufman, Paul L  
 APPLICANT: Liu, Xuyang  
 TITLE OF INVENTION: Method for Treating Glaucoma  
 FILE REFERENCE: 9601296\_00149  
 CURRENT APPLICATION NUMBER: US/11/060,920  
 CURRENT FILING DATE: 2005-02-18  
 PRIOR APPLICATION NUMBER: US 60/545,723  
 NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 5  
 LENGTH: 721  
 TYPE: PRT  
 ORGANISM: Clostridium botulinum  
 US-11-060-920-5

Query Match 4.6%; Score 83.5; DB 7; Length 721;  
 Best Local Similarity 20.9%; Pred. No. 3.1;  
 Matches 71; Conservative 39; Mismatches 117; Indels 113; Gaps 17;

Qy 2 KAIFVNAAPONTWAGGKLGMWSQHDITGFYG-----NGF-QNNNGPFRNDOLGAG 52  
 Db 165 KSKFIPN-----NTFSNAKIKANARDTDRGIPDEWEINGTYVMNQKAWDDKFAAN 219  
 Qy 53 AFGQQYN-----PYLGFBEMGFDWLGRNAYKGSVDN-----GAFKAQGVQ 92  
 Db 220 GYKKVSNPFKECTANDPTDFE-----KVSGOIDPSVSMVRDPMSAYPIVGVQ 270  
 Qy 93 ---LTAKLGYPTDDIYTRGGMWRADSKGNATSGVSRSENDTGSPVFAVGVEW 148  
 Db 271 MERLVVSKSETITGDT-----KSMSKSTSNTINTGAEVSGSLQLAGGIPP 320  
 Qy 149 AVTRDIASTRLEYQWNNNIGDAGTVGTRPDNGM-LSGVS-----VRFQQEADAPVYAPA 201  
 Db 321 VFSMASANYSHWTQNTSTVDDTTGBFSQQLSINTGESAYINPNRYNTGTAPPYNNVT 380  
 Qy 202 PAPAPEVATKHTFLKSVDLFNFNKATLKPEGOAL-----D 237  
 Db 381 PT-----TIVIDQSVATK-GOBSLIJDYLNPGGTPIIGERPMALNTMD 426  
 Qy 238 QI-----YTQLSNMDPKDGSAAVVLGTYDRIGSEA-YN 268  
 Db 427 QFSSRLIPINYNQLSID-NGTVMLSTSQTGNFAKYN 464

RESULT 13  
 US-10-495-664-3  
 Sequence 3, Application US/10495664

Publication No. US20050244416A1  
 APPLICANT: JING, JUNDIABM  
 TITLE OF INVENTION: BISPECIFIC ANTI-CD38 ANTIBODY MOLECULE  
 FILE REFERENCE: 034358-0801  
 CURRENT APPLICATION NUMBER: US10/495,664  
 CURRENT FILING DATE: 2004-05-12  
 PRIOR APPLICATION NUMBER: PCT/EP02/12545  
 PRIOR FILING DATE: 2002-11-09  
 PRIORITY NUMBER: DE 101 56 482.1  
 PRIORITY FILING DATE: 2001-11-12  
 NUMBER OF SEQ ID NOS: 3  
 SOFTWARE: PatentIn Ver. 3.3  
 SEQ ID NO: 3  
 LENGTH: 543  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 OTHER INFORMATION: Protein construct  
 US-10-495-664-3

Query Match 4.4%; Score 81; DB 1; Length 348;  
 Best Local Similarity 20.9%; Pred. No. 2; Mismatches 41; Indels 160; Gaps 2.2;  
 Matches 77; Conservative 77; Gapless 77;

Qy 12 KDNNTWAGGKLGWSQYHDTGFYNGFONNNNGPTRNDGAGAFCGGYQVNPNYLGFGMC 6.8  
 Db 75 KDNNGKNTLKK-AEQQKTEPKNNNSNTLG-----YNGLULGPTLKLKSDKV 122  
 Qy 69 -----YDWLGRMAYKGVDNG-----AFKAQGVQLTAKGY---- 99  
 Db 123 KIRKLINNLIDENTTFHNG-LEYNGKVGDPSPQVIKPGKEKTKFEVNQDSATIWHPHPS 181  
 Qy 100 PITDDLDIYTFLGGMMWRADS-KGNAYASTGVSRSEHDGTGVSPVFAGGVEWA TRD--IA 155  
 Db 182 ENPAK-QVNGLISGLLVIEDSKANNP-----SDTGKNDLP-----IIQDTKFVS 226  
 Qy 156 TRLEYQVNINNIGDAGTYG-TRDNGMILSLGVSYRFQGQDAAPVVAAPAPAPEVATKHFT 214  
 Db 227 KKLNYNSKTKD-BDGQTGDTVLVNGIVN-----PLTTKEEK 261

Qy 215 LKSDVLFNPNKATLKPGQALDQLTQLSMDPKDGSAVVLYGTYRIGSEAYNQOLSEK 274  
 Db 262 IRLRLI-----NGSNARD-LNKLSN-----NQSF---- 285  
 Qy 275 RAQSVDYLVAKGIPAKI-SARGMGESENPNVTGNTCDNVKARAALIDCLAPDRREI--- 330  
 Db 286 -----BYIASDG---GQLXNAKKLKEIN-----LAPSERKEIVID 317

Qy 331 --EVKGYK 336  
 Db 318 LSKMKGK 325

RESULT 15  
 US-10-802-796-728  
 Sequence 728, Application US/10802796  
 Publication No. US20050250104A1  
 GENERAL INFORMATION:  
 APPLICANT: COLE, STEWART  
 APPLICANT: BUCHREISER-BROSCHE, ROLAND  
 APPLICANT: GORDON, STEPHEN  
 APPLICANT: BILLAULT, ALAIN  
 TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST  
 TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC BASED  
 TITLE OF INVENTION: DNA LIBRARY, APPLICATION TO THE DETECTION OF  
 TITLE OF INVENTION: MYCOBACTERIA.  
 FILE REFERENCE: 05394\_0011-00000  
 CURRENT APPLICATION NUMBER: US/10/802,796  
 PRIORITY FILING DATE: 2004-03-18  
 PRIORITY APPLICATION NUMBER: US/09/673,476  
 PRIORITY FILING DATE: 2002-03-29  
 PRIORITY APPLICATION NUMBER: PCT/1B99/00740  
 PRIORITY FILING DATE: 1999-04-16  
 PRIORITY APPLICATION NUMBER: 09/060,756  
 NUMBER OF SEQ ID NOS: 743  
 SOFTWARE: PatentIn Ver. 2.2  
 SEQ ID NO: 728  
 LENGTH: 334  
 TYPE: PRT  
 ORGANISM: Mycobacterium sp.  
 US-10-802-796-728

Query Match 4.3%; Score 79; DB 1; Length 334;  
 Best Local Similarity 26.0%; Pred. No. 2.8; Mismatches 11; Indels 58; Gaps 8;  
 Matches 44; Conservative 44; Gapless 44;

Qy 18 AGGKLGLWSQYHDTGFY-GNGFONNNNGPTRNDGAGAFCGGYQVNPNYLGFGMC-YDNLGRM 75  
 Db 187 AGGAGG-----GJUGDGAGGNGLLSSGGAGGGGTAGGGVAGGNAGNAGNLFPG 240  
 Qy 76 A-----YKGSVDNGAFAKQGVQLTAKGYPITDDLIYTRLGGMVNRADSKGNYASSTGV 130

RESULT 14  
 Sequence 2866, Application US/10793626  
 Publication No. US20050255478A1  
 GENERAL INFORMATION:  
 APPLICANT: KIMMERLY, WILLIAM JOHN  
 TITLE OF INVENTION: STAPHYLOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
 FILE REFERENCE: PUS4800S  
 CURRENT APPLICATION NUMBER: US10/793,626  
 CURRENT FILING DATE: 2004-03-04  
 PRIOR APPLICATION NUMBER: 60/164,258  
 PRIOR FILING DATE: 1999-11-09  
 NUMBER OF SEQ ID NOS: 4472  
 SEQ ID NO: 2866  
 LENGTH: 348  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 OTHER INFORMATION: amino acid sequence  
 US-10-793-626-2866

Db	241	AGGIGGIGGGNANGGA GGNGT-----  :   :   :   :   :   :   :   :   :
Qy	131	RSEHDGTGVSPFAGGVENAVTRDIA TRLYQWVNINMIDAGTVGRPDNG 179
Db	279	LSGDTG-----  :   :   :   :   :   :   :   :   :   :   :   :   :
		-GSAGAIGTGCGG 304

Search completed: November 26, 2005, 00:21:22  
Job time : 11 secs

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GenCore version 5.1.6

OM protein - protein search, using SW mode!

Run on: November 25, 2005, 00:10:34 ; Search time 162 Seconds  
(without alignments)

887.243 Million cell updates/sec

Title: US-09-913-772A-2

Perfect score: 1823

Sequence: 1 MKAIFVNLNAPKONTWYAGG.....DRRVEIEVKGYKEVVTQPG 344

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1867568 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% ; Maximum Match 100%

Listing First 45 summaries

Database : Published Applications AA Main:\*

1: /cgns\_6/\_ptodata/1/\_pubpa/\_US07\_PUBCOMB.pep:\*

2: /cgns\_6/\_ptodata/1/\_pubpa/\_US08\_PUBCOMB.pep:\*

3: /cgns\_6/\_ptodata/1/\_pubpa/\_US09\_PUBCOMB.pep:\*

4: /cgns\_6/\_ptodata/1/\_pubpa/\_US10\_PUBCOMB.pep:\*

5: /cgns\_6/\_ptodata/1/\_pubpa/\_US10B\_PUBCOMB.pep:\*

6: /cgns\_6/\_ptodata/1/\_pubpa/\_US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1823	100.0	344	4 US-10-169-953-2	Sequence 2; Appli
2	1511	82.9	346	4 US-10-467-421-90	Sequence 90; Appli
3	1511	82.9	346	4 US-10-467-421-91	Sequence 97; Appli
4	1511	82.9	346	5 US-10-946-647-1413	Sequence 1413; Ap
5	1511	82.9	346	5 US-10-946-647-1448	Sequence 1448; Ap
6	1505	82.6	346	5 US-10-946-647-1424	Sequence 1424; Ap
7	1499	82.2	350	5 US-10-946-647-1377	Sequence 1377; Ap
8	1495	82.0	350	5 US-10-946-647-1389	Sequence 1389; Ap
9	1495	82.0	350	5 US-10-946-647-1395	Sequence 1395; Ap
10	1495	82.0	350	5 US-10-946-647-1404	Sequence 1404; Ap
11	754	41.4	190	4 US-10-416-708A-24	Sequence 24; Appli
12	754	41.4	192	4 US-10-416-708A-27	Sequence 27; Appli
13	748	41.0	194	4 US-10-416-708A-10	Sequence 10; Appli
14	748	41.0	194	4 US-10-416-708A-64	Sequence 64; Appli
15	719.5	39.5	161	5 US-10-946-647-1436	Sequence 1436; Ap
16	689	37.8	344	4 US-10-336-840-9	Sequence 9; Appli
17	688	37.7	344	4 US-10-336-840-6	Sequence 6; Appli
18	687	37.7	137	4 US-10-412-056-2	Sequence 2; Appli
19	687	37.7	153	3 US-09-905-176-22	Sequence 10; Appli
20	685	37.6	344	4 US-10-336-840-3	Sequence 3; Appli
21	684	37.5	344	4 US-10-336-840-1	Sequence 1; Appli
22	684	37.5	344	4 US-10-336-840-2	Sequence 2; Appli
23	684	37.5	344	4 US-10-336-840-4	Sequence 4; Appli
24	684	37.5	344	4 US-10-336-840-7	Sequence 7; Appli
25	683	37.5	344	4 US-10-336-840-10	Sequence 10; Appli
26	680.5	37.3	341	4 US-10-336-840-5	Sequence 5; Appli
27	680.5	37.3	341	4 US-10-336-840-8	Sequence 8; Appli

## ALIGNMENTS

RESULT 1  
US-10-169-953-2

; Sequence 2, Application US/10169953  
; Publication No. US20030044915A1

; GENERAL INFORMATION:

; APPLICANT: Thierry BAUSSANT  
; APPLICANT: Pascal JEANNIN  
; APPLICANT: Yves DELNESTE  
; APPLICANT: Francois LAMY  
; APPLICANT: Jean-Yves BONNEFOY

; TITLE OF INVENTION: METHOD FOR PREPARING A POLYPEPTIDE SOLUBLE IN AN AQUEOUS SOLVENT

; TITLE OF INVENTION: IN THE ABSENCE OF DETERGENT

; FILE REFERENCE: D18390

CURRENT APPLICATION NUMBER: US/10/169,953

CURRENT FILING DATE: 2002-07-03

PRIOR APPLICATION NUMBER: FR 00 000700

PRIOR FILING DATE: 2000-01-04

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 344

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

FEATURE: OTHER INFORMATION: P40

US-10-169-953-2

Query Match 100.0%; Score 1823; DB 4; Length 344;

Best Local Similarity 100.0%; Pred. No. 1 3e-160;

Matches 344; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MKAIFVNLNAPKDNTWYAGGKLGWSOYHDTGFGNGFQNNNGPTRNDLGAGAFGGTQVN 60

Dy 1 MKAIFVNLNAPKDNTWYAGGKLGWSOYHDTGFGNGFQNNNGPTRNDLGAGAFGGTQVN 60

Qy 2 PYLGFPMGYDNLGRMAYKGSVDNGAKAQGVOLTAKLGYPITDDLDLYTRLCGMVRADS 120

Dy 2 PYLGFPMGYDNLGRMAYKGSVDNGAKAQGVOLTAKLGYPITDDLDLYTRLCGMVRADS 120

Qy 3 KNYASTGVSRSEBDTGSPVFAGGGEAVTRDIATRLEYQVNNGDAGTVTRPDNGM 180

Dy 3 KNYASTGVSRSEBDTGSPVFAGGGEAVTRDIATRLEYQVNNGDAGTVTRPDNGM 180

Qy 4 1SLGVSYRFQGEDAAPVAP 240

Dy 4 1SLGVSYRFQGEDAAPVAP 240

Qy 5 1SLGVSYRFQGEDAAPVAP 240

Dy 5 1SLGVSYRFQGEDAAPVAP 240

**RESULT 2**  
US-10-467-421-90

Sequence 90, Application US/10467421  
Publication No. US20040116665A1

GENERAL INFORMATION:  
 APPLICANT: Berhet, Francois-Xavier Jacques  
 APPLICANT: Denoel, Philippe  
 APPLICANT: Neyt, Cecile Anne  
 APPLICANT: Poolman, Jan  
 APPLICANT: Thonnard, Joelle

TITLE OF INVENTION: Vaccine Composition

FILE REFERENCE: B45259

CURRENT APPLICATION NUMBER: US/10/467,421  
 CURRENT FILING DATE: 2003-08-08  
 PRIOR APPLICATION NUMBER: PCT/EP02/01361  
 PRIOR FILING DATE: 2002-02-08

PRIOR APPLICATION NUMBER: GB 0103171.5  
 PRIOR FILING DATE: 2001-02-08

NUMBER OF SEQ ID NOS: 98  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 90  
 LENGTH: 146  
 TYPE: PRT  
 ORGANISM: *E. coli*  
 US-10-467-421-90

Query Match 82.9%; Score 1511; DB 4; Length 346;  
 Best Local Similarity 84.9%; Pred. No. 1..3e-131;  
 Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;

Qy 6 VLNAAPKDNTWAGKLGWSQYHDTGPGNGFQNNNPTRDQLGAGAFGGVQVNPyLGF 65  
 Db 18 VQAQAPKDNTWYTGAKLGWSQYHDTGFI----NNNGPPTHENQLGAGAFGGVQVNPyVG 72

Qy 66 EMGYDWLGRMAYKGSYVDNGAFAKAQGVLTAKLGYPTTDDLDIYTRLGGMWFRADSKNYA 125  
 Db 73 EMGYDWLGRMPPKGSTENGAYKAQGVLTAKLGYPTTDDLDIYTRLGGMWFRADSKSN-- 130

Db 126 STGVSRSEHDTCVSVPYFAGGVWAVTRDIAATRLYEQVNNGIADACTVGRTPDNGMLSLGV 185  
 Db 131 --VYGRNHDTGCVSPVAGGYTAITPEIAATRLYEQVNNGIADACTVGRTPDNGMLSLGV 187

Qy 186 SYRFQGDAAPVVAAPAPAPAEVATKFTLSDVLNFNKATLKPECGQALDQLYTQSLN 245  
 Db 188 SYRFQGDAAPVVAAPAPAPAEVATKFTLSDVLNFNKATLKPECGQALDQLYTQSLN 247

Qy 246 MDPKDGSAAVVLGYTDIGSEAYNQOLSEKRAQSVDYLVAKGIPAGKISARGMGESENPTV 305  
 Db 248 LDPKDGSAAVVLGYTDIGSEAYNQOLSEKRAQSVDYLVAKGIPAGKISARGMGESENPTV 307

Qy 306 GNTCDNYKARALIDCLAPDRVEITVKGYKEVVTQP 342  
 Db 308 GNTCDNYKQRALIDCLAPDRVEEVKGIRKDVTQP 344

**RESULT 4**  
US-10-946-647-1413

Sequence 1413, Application US/10946647  
 Publication No. US20050186217A1

GENERAL INFORMATION:  
 APPLICANT: EMBRY, DARYLL A.  
 APPLICANT: STRAUB, DARREN E.  
 APPLICANT: WONDERLING, LAURA  
 TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE

CURRENT APPLICATION NUMBER: US/10/946,647  
 CURRENT FILING DATE: 2/04/09-20  
 PRIOR APPLICATION NUMBER: 60/504,119  
 PRIOR FILING DATE: 2003-09-19  
 NUMBER OF SEQ ID NOS: 1448  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO: 1413  
 LENGTH: 346  
 TYPE: PRT  
 ORGANISM: *Escherichia coli*  
 US-10-946-647-1413

Query Match 82.9%; Score 1511; DB 5; Length 346;  
 Best Local Similarity 84.9%; Pred. No. 1..3e-131;  
 Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;

Qy 6 VLNAAPKDNTWAGKLGWSQYHDTGPGNGFQNNNPTRDQLGAGAFGGVQVNPyLGF 65  
 Db 18 VQAQAPKDNTWYTGAKLGWSQYHDTGFI----NNNGPPTHENQLGAGAFGGVQVNPyVG 72

Qy 66 EMGYDWLGRMAYKGSDVNGAFAQGVOLTAKLGYPTDDIYTRILGMMWRADSKGNYA 125  
 Db 73 EMGYDWLGRMAYKGSDVNGAFAQGVOLTAKLGYPTDDIYTRILGMMWRADTSN- 130  
 Qy 126 STGVSRSBHDGTGSPVFGGVWAVTRDIATRLEYQWNNINGDAGTVTRPONGMSLG 185  
 Db 131 ---VYGNKHDTGSPVFGGVWAVTRPEATRLEYQWNNIGDAHTIGTRPONGMSLG 187  
 Qy 186 SYRFQEDAIVVAPAPAPEVAKHFTLKSVDLFNFNKATLKPEGQALDOLYTOLSN 245  
 Db 188 SYRFQEDAIVVAPAPAPEVQTKHFTLKSVDLFNFNKATLKPEGQALDOLYQSLSN 247  
 Qy 246 MDPKDGSAVVLGYTDRIGSEAQNQLSERKRAQSVDYLVAKGTPAKISARGMGESENVT 305  
 Db 248 LDPKDGSAVVLGYTDRIGSDAYNQGLSERKRAQSVDYLVAKGTPAKISARGMGESENVT 307  
 Db 306 GNTCDNYVKARAALIDCLAPDRRVEIEVKGYKEVVTQ 342  
 Db 308 GNTCDNYVKARAALIDCLAPDRRVEIEVKGYKDVTQ 344  
 Db

**RESULT 5**  
 US-10-946-647-1448  
 / Sequence 1448, Application US/10946647  
 / Publication No. US20050186217A1  
 / GENERAL INFORMATION:  
 / APPLICANT: STRAUB, DARREN E.  
 / APPLICANT: WONDERLING, LAURA  
 / TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE  
 / FILE REFERENCE: 293\_00340101  
 / CURRENT APPLICATION NUMBER: US/10/946\_647  
 / CURRENT FILING DATE: 2004-09-20  
 / PRIOR APPLICATION NUMBER: 60/504,119  
 / PRIOR FILING DATE: 2003-09-19  
 / NUMBER OF SEQ ID NOS: 1448  
 / SOFTWARE: Patentin version 3.3  
 / SEQ ID NO 1448  
 / LENGTH: 346  
 / TYPE: PRT  
 / ORGANISM: Escherichia coli

Query Match 82.9%; Score 1511; DB 5; Length 346;  
 Best Local Similarity 84.9%; Prod. No. 1..3e-11; Indels 10; Gaps 2;  
 Matches 286; Conservative 17; Mismatches 24;  
 Qy 6 VLNAAPKDNNTWAGKLUGWSQYHDTGIFTDGYNGFQNNNGPTRNDLGAGAFGGYQVNPNPLG 65  
 Db 18 VQAAPKDNNTWAGKLUGWSQYHDTGIFTDGYNGFQNNNGPTHENOLGAGAFGGYQVNPNVVG 72  
 Qy 66 ENGYDWLGRMAYKGSDVNGAFAQGVOLTAKLGYPTDDIYTRILGMMWRADSKGNYA 125  
 Db 73 ENGYDWLGRMAYKGSDVNGAFAQGVOLTAKLGYPTDDIYTRILGMMWRADTSN- 130  
 Qy 126 STGVSRSBHDGTGSPVFGGVWAVTRPEATRLEYQWNNINGDAGTVTRPONGMSLG 185  
 Db 131 ---VYGNKHDTGSPVFGGVWAVTRPEATRLEYQWNNINGDAGTVTRPONGMSLG 187  
 Qy 186 SYRFQEDAIVVAPAPAPEVAKHFTLKSVDLFNFNKATLKPEGQALDOLYTOLSN 245  
 Db 188 SYRFQEDAIVVAPAPAPEVQTKHFTLKSVDLFNFNKATLKPEGQALDOLYQSLSN 247  
 Db

**RESULT 7**  
 US-10-946-647-1377  
 / Sequence 1377, Application US/10946647  
 / Publication No. US20050186217A1  
 / GENERAL INFORMATION:  
 / APPLICANT: STRAUB, DARREN E.  
 / APPLICANT: WONDERLING, LAURA  
 / TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE  
 / FILE REFERENCE: 293\_00340101  
 / CURRENT APPLICATION NUMBER: US/10/946\_647  
 / CURRENT FILING DATE: 2004-09-20  
 / PRIOR APPLICATION NUMBER: 60/504,119  
 / PRIOR FILING DATE: 2003-09-19  
 / NUMBER OF SEQ ID NOS: 1448  
 / SOFTWARE: Patentin version 3.3  
 / SEQ ID NO 1377  
 / LENGTH: 350  
 / TYPE: PRT  
 / ORGANISM: Salmonella enterica

Query Match 82.2%; Score 1499; DB 5; Length 350;  
 US-10-946-647-1377

Best Local Similarity 82.8%; Pred. No. 1.8e-130; Indels 6; Gaps 2; Matches 279; Conservative 26; Mismatches 26; Gaps 2; Qy 6 VLNAPKONTWYAGKLGIKQYHDGTGFIYNGFQNNGPRTNDLGAFFGQVNPYLG F 65 Db 18 VAQAPKONTWYAGKLGIKQYHDGTGFI----HNDGPTHENOLGAGAFFGQVNPYVG F 72

RESULT 9  
US-10-946-647-1395

; Sequence 1395, Application US/10946647  
; Publication No. US20050186217A1  
; GENERAL INFORMATION:  
; APPLICANT: EMERY, DARYLL A.  
; APPLICANT: STRAUB, DARREN B.  
; APPLICANT: WONDERLING, LAURA  
; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE  
; FILE REFERENCE: 293.00340101  
; CURRENT APPLICATION NUMBER: US/10/946,647  
; PRIORITY APPLICATION NUMBER: 60/504,119  
; PRIORITY FILING DATE: 2004-09-20  
; NUMBER OF SEQ ID NOS: 1448  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 1395  
; LENGTH: 350  
; TYPE: PRT  
; ORGANISM: *Salmonella enterica*  
US-10-946-647-1395

Query Match 82.0%; Score 1495; DB 5; Length 350;  
Best Local Similarity 82.8%; Pred. No. 4.1e-130; Indels 6; Gaps 2; Matches 279; Conservative 26; Mismatches 26; Gaps 2; Qy 6 VLNAPKONTWYAGKLGIKQYHDGTGFIYNGFQNNGPRTNDLGAFFGQVNPYLG F 65 Db 18 VAQAPKONTWYAGKLGIKQYHDGTGFI----HNDGPTHENOLGAGAFFGQVNPYVG F 72

RESULT 8  
US-10-946-647-1389

; Sequence 1389, Application US/10946647  
; Publication No. US20050186217A1  
; GENERAL INFORMATION:  
; APPLICANT: EMERY, DARYLL A.  
; APPLICANT: STRAUB, DARREN E.  
; APPLICANT: WONDERLING, LAURA  
; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE  
; FILE REFERENCE: 293.00340101  
; CURRENT APPLICATION NUMBER: US/10/946,647  
; CURRENT FILING DATE: 2004-09-20  
; PRIORITY APPLICATION NUMBER: 60/504,119  
; PRIORITY FILING DATE: 2003-09-19  
; NUMBER OF SEQ ID NOS: 1448  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 1389  
; LENGTH: 350  
; TYPE: PRT  
; ORGANISM: *Salmonella enterica*  
US-10-946-647-1389

Query Match 82.0%; Score 1495; DB 5; Length 350;  
Best Local Similarity 82.8%; Pred. No. 4.1e-130; Indels 6; Gaps 2; Matches 279; Conservative 26; Mismatches 26; Gaps 2; Qy 6 VLNAPKONTWYAGKLGIKQYHDGTGFIYNGFQNNGPRTNDLGAFFGQVNPYLG F 65 Db 18 VAQAPKONTWYAGKLGIKQYHDGTGFI----HNDGPTHENOLGAGAFFGQVNPYVG F 72

RESULT 10  
US-10-946-647-1404

; Sequence 1404, Application US/10946647  
; Publication No. US20050186217A1  
; GENERAL INFORMATION:  
; APPLICANT: STRAUB, DARREN B.  
; APPLICANT: WONDERLING, LAURA  
; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE  
; FILE REFERENCE: 293.00340101  
; CURRENT APPLICATION NUMBER: US/10/946,647  
; CURRENT FILING DATE: 2004-09-20  
; PRIORITY APPLICATION NUMBER: 60/504,119  
; PRIORITY FILING DATE: 2003-09-19  
; NUMBER OF SEQ ID NOS: 1448  
; SOFTWARE: PatentIn version 3.3

SEQ ID NO 1404  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Salmonella enterica  
Query Match 82.0%; Score 1495; DB 5; Length 350;  
Best Local Similarity 82.8%; Pred. No. 4.1e-130;  
Matches 2/9; Conservative 26; Mismatches 26; Indels 6; Gaps 2;

Qy 6 VLNAAPKONTWYAGGKLIGMSQYHDTGPFYNGFQNNGPTRNDLGAGAAGGGQVNPNPLGF 65  
Db 18 VAQAAPKONTWYAGAKLGSQYHDTGFI----HNDGPHTENQLGAGAAGGGQVNPNPVGF 72  
Qy 66 EMGYDWLGRMAYKGSDVNDNAFKAGGVQLTAKLGPITDLDIYTRLGMWWRADSKNYA 125  
Qy 73 STGVRSRSEDTGVSPPVFAGGVEAVTRDIAATRLYEQWNINIDAGTVTRPDNGMLSLGV 185  
Qy 126 STGVRSRSEDTGVSPPVFAGGVEAVTRDIAATRLYEQWNINIDAGTVTRPDNGMLSLGV 132  
Db 133 G-GPSTKDHDGTGVSPPVFAGGVEAVTRDIAATRLYEQWNINIDAGTVTRPDGLLSGV 191

Qy 186 SYRFQQEDDAPVYAAPAAPAPEYATKHEFLKSDVLFNENKATLKPEGOALDOLYQTLSN 245  
Db 192 SYRFQQEAPVYAAPAAPAPEYATKHEFLKSDVLFNENKSTLKPEGOALDOLYSQLSN 251  
Qy 246 MDPKDGSAVVLGYTDRIGSEAYAQNLSERAQSVDYLAKGIPAGKISARGNGESNPVT 305  
Db 252 LDPKDGSVTVLGFTRDSSDAYNQGLSERAAQSVDYLISKGPDSKISARGNGESNPVT 311  
Qy 306 GNTCDNVKRAALIDCLADPDRVEIEVKYKEYVTTQ 342  
Db 312 GNTCDNVKRAALIDCLADPDRVEIEVKYKEYVTTQ 348

RESULT 11  
US-10-416-708A-24  
; Sequence 24, Application US/10416708A  
; Publication No. US20040161753A1  
; GENERAL INFORMATION:  
; APPLICANT: Wisse, John G.  
; TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING  
; TITLE REFERENCE: 37719-0004  
; CURRENT APPLICATION NUMBER: US/10/416,708A  
; CURRENT FILING DATE: 2004-01-28  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 24  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-416-708A-24  
Query Match 41.4%; Score 754; DB 4; Length 190;  
Best Local Similarity 79.9%; Pred. No. 1.3e-61;  
Matches 139; Conservative 9; Mismatches 16; Indels 10; Gaps 2;

Qy 6 VLNAAPKONTWYAGGKLIGMSQYHDTGPFYNGFQNNGPTRNDLGAGAAGGGQVNPNPLGF 65  
Db 20 VAQAAPKONTWYAGKLGSQYHDTGFI----HNDGPHTENQLGAGAAGGGQVNPNPVGF 74  
Qy 66 EMGYDWLGRMAYKGSDVNDNAFKAGGVQLTAKLGPITDLDIYTRLGMWWRADSKNYA 125  
Db 75 EMGYDWLGRMAYKGSDVNDNAFKAGGVQLTAKLGPITDLDIYTRLGMWWRADSKNYA 132

Qy 126 STGVRSRSEDTGVSPPVFAGGVEAVTRDIAATRLYEQWNINIDAGTVTRPDNG 179  
Db 133 ---VYGRNHDTGVSPPVFAGGVEAVTRDIAATRLYEQWNINIDAGTVTRPDNG 183  
Db 75 EMGYDWLGRMAYKGSDVNDNAFKAGGVQLTAKLGPITDLDIYTRLGMWWRADSKNYA 125  
Db 75 EMGYDWLGRMAYKGSDVNDNAFKAGGVQLTAKLGPITDLDIYTRLGMWWRADSKNYA 132

RESULT 12  
US-10-416-708A-27  
; Sequence 27, Application US/10416708A  
; Publication No. US20040161753A1  
; GENERAL INFORMATION:  
; APPLICANT: Fromknecht, Katja  
; APPLICANT: Wisse, John G.  
; TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING  
; FILE REFERENCE: 37719-0004  
; CURRENT APPLICATION NUMBER: US/10/416,708A  
; CURRENT FILING DATE: 2004-01-28  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 27  
; LENGTH: 192  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-416-708A-27  
Query Match 41.4%; Score 754; DB 4; Length 192;  
Best Local Similarity 79.9%; Pred. No. 1.3e-61;  
Matches 139; Conservative 9; Mismatches 16; Indels 10; Gaps 2;

Qy 6 VLNAAPKONTWYAGGKLIGMSQYHDTGPFYNGFQNNGPTRNDLGAGAAGGGQVNPNPLGF 65  
Db 20 VAQAAPKONTWYAGKLGSQYHDTGFI----HNDGPHTENQLGAGAAGGGQVNPNPVGF 74  
Qy 66 EMGYDWLGRMAYKGSDVNDNAFKAGGVQLTAKLGPITDLDIYTRLGMWWRADSKNYA 125  
Db 75 EMGYDWLGRMAYKGSDVNDNAFKAGGVQLTAKLGPITDLDIYTRLGMWWRADSKNYA 132

Qy 126 STGVRSRSEDTGVSPPVFAGGVEAVTRDIAATRLYEQWNINIDAGTVTRPDNG 179  
Db 133 ---VYGRNHDTGVSPPVFAGGVEAVTRDIAATRLYEQWNINIDAGTVTRPDNG 183  
Db 75 EMGYDWLGRMAYKGSDVNDNAFKAGGVQLTAKLGPITDLDIYTRLGMWWRADSKNYA 125  
Db 75 EMGYDWLGRMAYKGSDVNDNAFKAGGVQLTAKLGPITDLDIYTRLGMWWRADSKNYA 132

RESULT 13  
US-10-416-708A-10  
; Sequence 10, Application US/10416708A  
; Publication No. US20040161753A1  
; GENERAL INFORMATION:  
; APPLICANT: Fromknecht, Katja  
; APPLICANT: Wisse, John G.  
; TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING  
; FILE REFERENCE: 37719-0004  
; CURRENT APPLICATION NUMBER: US/10/416,708A  
; CURRENT FILING DATE: 2004-01-28  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 10  
; LENGTH: 194  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-416-708A-10  
Query Match 41.0%; Score 748; DB 4; Length 194;  
Best Local Similarity 79.8%; Pred. No. 4.9e-61;  
Matches 138; Conservative 9; Mismatches 16; Indels 10; Gaps 2;

Qy 6 VLNAAPKONTWYAGGKLIGMSQYHDTGPFYNGFQNNGPTRNDLGAGAAGGGQVNPNPLGF 65  
Db 20 VAQAAPKONTWYAGKLGSQYHDTGFI----HNDGPHTENQLGAGAAGGGQVNPNPVGF 74  
Qy 66 EMGYDWLGRMAYKGSDVNDNAFKAGGVQLTAKLGPITDLDIYTRLGMWWRADSKNYA 125  
Db 75 EMGYDWLGRMAYKGSDVNDNAFKAGGVQLTAKLGPITDLDIYTRLGMWWRADSKNYA 132

Qy 126 STGVRSRSEDTGVSPPVFAGGVEAVTRDIAATRLYEQWNINIDAGTVTRPDNG 179  
Db 133 ---VYGRNHDTGVSPPVFAGGVEAVTRDIAATRLYEQWNINIDAGTVTRPDNG 183  
Db 75 EMGYDWLGRMAYKGSDVNDNAFKAGGVQLTAKLGPITDLDIYTRLGMWWRADSKNYA 125  
Db 75 EMGYDWLGRMAYKGSDVNDNAFKAGGVQLTAKLGPITDLDIYTRLGMWWRADSKNYA 132

Qy 126 STGVSRSSEHDGTGSPVAGGVENAVTRDIASTRLEYQWVNINIGDAGTVGRPDN 178  
 Db 133 ---VYGRNHDGTGSPVAGGVENAVTRPEIATRLEYQWVNINIGDAHTIGTRPDN 182

RESULT 14  
 US-10-416-708A-64  
 Sequence 64, Application US/10416708A  
 Publication No. US20040161753A1  
 GENERAL INFORMATION:  
 APPLICANT: Wies, John G.  
 Fromknecht, Katja  
 TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING  
 SPECIFICITIES  
 FILE REFERENCE: 37779-0004  
 CURRENT APPLICATION NUMBER: US/10/416,708A  
 CURRENT FILING DATE: 2004-01-28  
 NUMBER OF SEQ ID NOS: 89  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO: 64  
 LENGTH: 194  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic Construct

US-10-416-708A-64

Query Match Score 748; DB 4; Length 194;  
 Best Local Similarity 79.8%; Pred. No. 4.9e-61; Length 194;  
 Matches 138; Conservative 9; Mismatches 16; Indels 10; Gaps 2;

Qy 6 VLNAPKONTWYAGGKLIGNSQYHDGTGFYQNGFQNNGPRTNRDOLGAGAFGGYQVNPILG  
 Db 20 VAQQAKPDKNTWYTGAKLGSQYHDGTGF1----NNNGPTHEQNLGAGAFGGQVNPIVG F 74

Qy 66 EMGYDWLGMAKGSUDNGAFKAQGVOLTAKLGYPTIDLDYTRUGMWMADSKNYA 125  
 Db 75 EMGYDWLGMPYKGSSVNGAFKAQGVOLTAKLGYPTIDLDYTRUGMWMADSKNYA 132

Qy 126 STGVSRSSEHDGTGSPVAGGVENAVTRDIASTRLEYQWVNINIGDAGTVGRPDN 178  
 Db 133 ---VYGRNHDGTGSPVAGGVENAVTRPEIATRLEYQWVNINIGDAHTIGTRPDN 182

RESULT 15  
 US-10-946-647-1436  
 Sequence 1436 Application US/10946647  
 Publication No. US20050186217A1  
 GENERAL INFORMATION:  
 APPLICANT: EMBRY, DARYL A.  
 APPLICANT: STRAUB, DARREN E.  
 APPLICANT: WONDERLING, LAURA  
 TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE  
 FILE REFERENCE: 93\_00340101  
 CURRENT APPLICATION NUMBER: US/10/946,647  
 CURRENT FILING DATE: 2004-09-20  
 PRIOR APPLICATION NUMBER: 60/504,119  
 PRIOR FILING DATE: 2003-09-19  
 NUMBER OF SEQ ID NOS: 1448  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO: 1436  
 LENGTH: 161  
 TYPE: PRT  
 ORGANISM: Escherichia coli

US-10-946-647-1436

Query Match Score 719.5; DB 5; Length 161;  
 Best Local Similarity 84.6%; Pred. No. 1.7e-58;  
 Matches 137; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

Qy 103 DDLDIYTRLGGMWYRADSKNYASTGVSRSSEHDGTGSPVAGGVENAVTRDIATRLEYQW 162



The membrane fraction is used for treatment and prevention of cancer (particularly of the bladder, prostate, colon or liver) and also malignant melanoma.

**Sequence 344 AA;**

Query Match 100.0%; Score 1823; DB 3; Length 344;  
Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

Matches 344; Conservative 0; Mismatches 0; Gaps 0;

SQ 1 MKAIFLVNAAPKDNTWYACKLGWSQYHDTGFYGNQFONNNPTRNDOLGAGAFGGTQVN 60

2 MKAIFLVNAAPKDNTWYACKLGWSQYHDTGFYGNQFONNNPTRNDOLGAGAFGGTQVN 60

3 PYLGFEMGYDWLGRMAYKGSVDNGAFKAQVQLTAKTGYPTIDLDIYTBLGMMWRADS 120

4 PYLGFEMGYDWLGRMAYKGSVDNGAFKAQGVOLTAKLGYPTIDLDIYTBLGMMWRADS 120

5 QY 61 KGNYASTGVRSERHDGTGSPVPGGGVEMAVTDLATRLEYQWNNIIGDTGVTRPQMG 180

61 KGNYASTGVRSERHDGTGSPVPGGGVEMAVTDLATRLEYQWNNIIGDTGVTRPQMG 180

62 DB 121 KGNYASTGVRSERHDGTGSPVPGGGVEMAVTDLATRLEYQWNNIIGDTGVTRPQMG 180

61 KGNYASTGVRSERHDGTGSPVPGGGVEMAVTDLATRLEYQWNNIIGDTGVTRPQMG 180

63 QY 181 LSLGVSYRFQEDAAPVYAPAPAPEVAKHTFLKSVDLFNFNKATLKPEQOALDQLY 240

61 LSLGVSYRFQEDAAPVYAPAPAPEVAKHTFLKSVDLFNFNKATLKPEQOALDQLY 240

64 DB 181 LSLGVSYRFQEDAAPVYAPAPAPEVAKHTFLKSVDLFNFNKATLKPEQOALDQLY 240

61 QY 241 TQLSNMDPKDGSAVLYGTDRTGSEAYNQQLSEKRAQSVDYLVAKGIPACKISAPGMGE 300

61 DB 241 TQLSNMDPKDGSAVLYGTDRTGSEAYNQQLSEKRAQSVDYLVAKGIPACKISAPGMGE 300

62 QY 301 SNPVTGNTCDNVKARAALIDCLAPDRRVIEVKYKEVTTQPG 344

61 DB 301 SNPVTGNTCDNVKARAALIDCLAPDRRVIEVKYKEVTTQPG 344

63 QY 241 TQLSNMDPKDSAVVGYTRIGSEAYNQQLSEKRAQSVDYLVAKGIPACKISARGMGE 300

61 DB 241 TQLSNMDPKDSAVVGYTRIGSEAYNQQLSEKRAQSVDYLVAKGIPACKISARGMGE 300

64 QY 301 SNPVTGNTCDNVKARAALIDCLAPDRRVIEVKYKEVTTQPG 344

61 DB 301 SNPVTGNTCDNVKARAALIDCLAPDRRVIEVKYKEVTTQPG 344

65 DE RESULT 3  
AAV93341

ID AAV93341 Standard; protein: 344 AA.

XX XX XX AC AAV93341;

DT DT 04-SEP-2000 (first entry)

XX XX XX OS Klebsiella pneumoniae.

XX WO200018628-A1.

XX DR 24-AUG-2000.

XX PR 17-FEB-2000; 2000WO-FR000393.

XX PR 17-FEB-1999; 99FR-00001917.

XX PA (FABR ) FABRE MEDICAMENT SA PIERRE.

XX PI Renno T, Bonnefoy J;

XX DR WPI; 2000-543367/49.

XX DR N-PSDB; AAA3917.

XX PT Use of enterobacterial outer membrane protein A in vaccines for inducing

PT cytotoxic T cell responses, useful for treating or preventing infections

PT and tumors.

XX PS Claim 7; Page 38-39; 45pp; French.

XX CC The present sequence represents a Klebsiella pneumoniae outer membrane

CC protein A (OmpA), designated P40. The enterobacterial OmpA polypeptide, or its fragments, is used for preparing a composition that induces, or increases, the cytotoxic T cell (CTL) response against an infectious agent or tumour cell. Compositions containing OmpA, optionally mixed with or coupled to a suitable antigen or hapten, are used as vaccines for treatment or prevention of infections caused by viruses, bacteria, fungi and parasites or tumors, particularly where associated with an antigen and specifically melanoma. Nucleic acids that encode OmpA (or its fusion with antigens or haptons) are useful as genetic vaccines again for treating infections and tumors

XX Sequence 344 AA;

DB Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Sequence 344 AA;

DB Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823; DB 3; Length 344;

DB Best Local Similarity 100.0%; Pred. No. 1.3e-17; Indels 0; Gaps 0;

DB Matches 344; Conservative 0; Mismatches 0; Gaps 0;

DB CC Query Match 100.0%; Score 1823;

DR N-PSDB; AAA15498.  
 XX Use of enterobacterial outer membrane protein A for delivering active  
 PT substances, particularly immunogens for treating or preventing e.g.  
 PT cancer, to antigen presenting cells.  
 XX  
 PS Claim 9; Page 28-29; 35pp; French.

XX The present sequence represents a P40 protein. The protein is an outer  
 CC membrane protein A (OmpA). The protein is used in pharmaceutical  
 CC compositions for specific targeting of an active substance to antigen-  
 CC presenting cells (APCs), especially dendritic cells. OmpA binds  
 CC specifically to APCs and is internalized by them (in contrast to other  
 CC protein carriers such as tetanus toxoid). The OmpA protein is used to  
 CC deliver an antigen or hapten to modify (specifically to improve) an  
 CC immune response, especially for treatment or prevention of cancers  
 CC (particularly those that express associated antigen),  
 CC autoimmune disease, allergy, graft rejection, cardiovascular or central  
 CC nervous system diseases, inflammation, infection or immune deficiency  
 XX Sequence 344 AA;

Query Match 100.0%; Score 1823; DB 3; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-157;  
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MKAIFVLAAPKDNTWYAGKLGWSQYHDTGFYNGFONNNGPTRNDOLGAGAEGGYQVN 60  
 1 MKAIFVLAAPKDNTWYAGKLGWSQYHDTGFYNGFONNNGPTRNDOLGAGAEGGYQVN 60  
 Qy 61 PYLGFEMGYDWLGRMAYKGSDVNGAFKAQGVOLTAKUGYPTTDDLDIYTRLGGMVNRADS 120  
 Db 61 PYLGFEMGYDWLGRMAYKGSDVNGAFKAQGVOLTAKUGYPTTDDLDIYTRLGGMVNRADS 120  
 Qy 61 PYLGFEMGYDWLGRMAYKGSDVNGAFKAQGVOLTAKUGYPTTDDLDIYTRLGGMVNRADS 120  
 Db 61 PYLGFEMGYDWLGRMAYKGSDVNGAFKAQGVOLTAKUGYPTTDDLDIYTRLGGMVNRADS 120  
 Qy 121 KGNYASTGVSRSRSEHDGTGSPVFAAGGVWAVTRDIATLEYQWVNNGDAGTVGTRPDNGM 180  
 Db 121 KGNYASTGVSRSRSEHDGTGSPVFAAGGVWAVTRDIATLEYQWVNNGDAGTVGTRPDNGM 180  
 Qy 181 LSLGVSTRFGQDAAPVAPPAPAPAPEVATKHTLKSVDLFNFKATLKPEQQALDQLY 240  
 Db 181 LSLGVSTRFGQDAAPVAPPAPAPAPEVATKHTLKSVDLFNFKATLKPEQQALDQLY 240  
 Qy 241 TOLSNDMPDGSAVVLGYTDIGSEAYNQLSEKRAQSVDYLVAKGIPAGKISARGMGE 300  
 Db 241 TOLSNDMPDGSAVVLGYTDIGSEAYNQLSEKRAQSVDYLVAKGIPAGKISARGMGE 300  
 Qy 301 SNPVTGNTCDNVTKARAALIDCLAPDRRVIEVKGYKEVTTQPG 344  
 Db 301 SNPVTGNTCDNVTKARAALIDCLAPDRRVIEVKGYKEVTTQPG 344  
 Qy 301 SNPVTGNTCDNVTKARAALIDCLAPDRRVIEVKGYKEVTTQPG 344  
 Db 301 SNPVTGNTCDNVTKARAALIDCLAPDRRVIEVKGYKEVTTQPG 344

RESULT 4  
 AAB08825 standard; protein; 344 AA.  
 XX  
 AC AAB08825;  
 XX DT 02-JAN-2001 (first entry)  
 XX DE A P40 polypeptide (an outer membrane protein A (OmpA)).

XX P40; outer membrane protein A; OmpA; immunogen; cytokine; growth factor;  
 KW hormone; tumour-specific marker; vaccine; cancer; contraceptive.  
 XX OS Klebsiella pneumoniae.  
 XX PN FR2789902-A1.  
 XX PD 25-AUG-2000.  
 XX PF 24-FEB-1999; 99FR-00002314.  
 XX PR 24-FEB-1999; 99FR-00002314.

XX (PABR ) FABRE MEDICAMENT SA PIERRE.  
 PA XX PI Goetsch L, Corvaia N, Beck A, Haeuw JF, Bonnefoy JY;  
 PT XX DR WPI: 2000-573921/54.  
 PT DR N-PSDB; AAA75036.  
 XX PT Use of enterobacterial outer membrane protein as immunogenic carrier,  
 PT particularly for contraceptive and anti-cancer vaccines, provides strong  
 PT PT particular response.  
 XX PS Claim 5; Page 23-24; 34pp; French.  
 XX PS The present sequence represents a P40 polypeptide of Klebsiella  
 CC pneumoniae. P40 is an enterobacterial outer membrane protein A (OmpA). It  
 CC can be associated an immunogen, and used to prepare a pharmaceutical  
 CC composition for improving the immunological response to the immunogen.  
 CC The immunogen is selected from cytokines, growth factors or hormones (or  
 CC their receptors) and/or tumour-specific markers. Compositions containing  
 CC OmpA induce a strong and specific antibody response. The compositions of  
 CC the invention are especially useful in vaccines to prevent or treat  
 CC cancer or as contraceptives.  
 XX SQ Sequence 344 AA;  
 Query Match 100.0%; Score 1823; DB 3; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-157;  
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MKAIFVLAAPKDNTWYAGKLGWSQYHDTGFYNGFONNNGPTRNDOLGAGAEGGYQVN 60  
 1 MKAIFVLAAPKDNTWYAGKLGWSQYHDTGFYNGFONNNGPTRNDOLGAGAEGGYQVN 60  
 Db 61 PYLGFEMGYDWLGRMAYKGSDVNGAFKAQGVOLTAKUGYPTTDDLDIYTRLGGMVNRADS 120  
 61 PYLGFEMGYDWLGRMAYKGSDVNGAFKAQGVOLTAKUGYPTTDDLDIYTRLGGMVNRADS 120  
 Qy 121 KGNYASTGVSRSRSEHDGTGSPVFAAGGVWAVTRDIATLEYQWVNNGDAGTVGTRPDNGM 180  
 Db 121 KGNYASTGVSRSRSEHDGTGSPVFAAGGVWAVTRDIATLEYQWVNNGDAGTVGTRPDNGM 180  
 Qy 181 LSLGVSTRFGQDAAPVAPPAPAPAPEVATKHTLKSVDLFNFKATLKPEQQALDQLY 240  
 Db 181 LSLGVSTRFGQDAAPVAPPAPAPAPEVATKHTLKSVDLFNFKATLKPEQQALDQLY 240  
 Qy 241 TOLSNDMPDGSAVVLGYTDIGSEAYNQLSEKRAQSVDYLVAKGIPAGKISARGMGE 300  
 Db 241 TOLSNDMPDGSAVVLGYTDIGSEAYNQLSEKRAQSVDYLVAKGIPAGKISARGMGE 300  
 Qy 301 SNPVTGNTCDNVTKARAALIDCLAPDRRVIEVKGYKEVTTQPG 344  
 Db 301 SNPVTGNTCDNVTKARAALIDCLAPDRRVIEVKGYKEVTTQPG 344  
 Qy 301 SNPVTGNTCDNVTKARAALIDCLAPDRRVIEVKGYKEVTTQPG 344  
 Db 301 SNPVTGNTCDNVTKARAALIDCLAPDRRVIEVKGYKEVTTQPG 344

RESULT 5  
 AAB18804  
 ID AAB18804 standard; protein; 344 AA.  
 XX AC AAB18804;  
 XX DT 22-JAN-2001 (first entry)  
 XX DE A Klebsiella pneumoniae P40 polypeptide.  
 KW KW P40 polypeptide; membrane fraction; antigen; hapten; immune response;  
 KW KW infectious disease; cancer; paramyxovirus infection;  
 KW KW respiratory syncytial virus; parainfluenza.  
 XX OS Klebsiella pneumoniae.  
 XX PN WO200054789-A1.



DE Amino acid sequence of an outer membrane protein A, P40.  
 XX Outer membrane protein A; P40; antigen presenting cell; vaccine;  
 KW antiviral; antibacterial; anticancer; autoimmune disease; inflammation;  
 KW graft rejection; cardiovascular disease; immune deficiency.  
 XX Klebsiella pneumoniae.  
 OS Klebsiella pneumoniae.  
 PN FR2803302-A1.  
 XX DT 11-JUN-2001 (first entry)  
 XX XX  
 PD Amino acid sequence of an outer membrane protein A (OmpA) P40.  
 XX DE XX  
 XX ID AAB67770 standard; protein; 344 AA.  
 XX AC AAB67770;  
 XX DT 11-JUN-2001 (first entry)  
 XX XX  
 PF Outer membrane protein A; OmpA; P40; enterobacteria; nasal composition;  
 KW respiratory syncytial virus; RSV; RSV infection; lung; respiratory tract;  
 KW vaccine.  
 XX XX  
 PR (FABR ) OS Klebsiella pneumoniae.  
 XX OS  
 XX PN WO200121203-A1.  
 XX PN  
 PA 29-MAR-2001.  
 XX PD DR N-PSDB; AAH74731.  
 XX XX  
 PT 22-SEP-2000; 2000WO-FR002626.  
 PT XX  
 PR 23-SEP-1999; 99FR-00011888.  
 XX XX  
 PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
 XX XX  
 PA Corvatae N, Goestch L;  
 XX PI DR WPI: 2001-257929/26.  
 XX DR N-PSDB; AAH80152.  
 XX XX  
 PT Vaccine against respiratory syncytial virus, comprises enterobacterial  
 PT outer membrane protein and viral immunogen, provides protective response  
 PT throughout the respiratory tract.  
 XX XX  
 PS Claim 3; Page 28-29; 39pp; French.  
 XX XX  
 CC The present sequence represents an outer membrane protein A (P40) of  
 CC Klebsiella pneumoniae. The protein is soluble in aqueous solvent in  
 absence of detergent. The specification describes a method for the  
 preparation of this polypeptide. The P40 protein binds selectively to  
 CC antigen-presenting cell, so provides targeting, proliferation and/or  
 CC expression of molecules by these cells. P40 is used, alone or as an  
 CC adjuvant, to produce therapeutic compositions that are soluble in absence  
 CC of detergent, especially when formulated with an antigen or haptan for  
 CC modulating the host's immune system. Especially, it is used to prepare  
 CC vaccines, especially antiviral, antibacterial or anticancer (e.g. against  
 CC human immune deficiency virus, respiratory syncytial virus, measles,  
 CC mumps, tuberculosis etc.), but also against fungi, parasites, autoimmune  
 CC diseases, graft rejection, cardiovascular disease, inflammation and  
 CC immune deficiency.  
 XX Sequence 344 AA:  
 SQ Every Match Score 100.0%; Score 1823; DB 4; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-157;  
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Sequence 344 AA:  
 1 MKAIFVLAAPKDNTWYAGKUGLWSQYHDTGFYNGNQNNNPTTRNDQLGAGAFGGYQVN 60  
 1 MKAIFVLAAPKDNTWYAGKLGWSQYHDTGFYNGNQNNNPTTRNDQLGAGAFGGYQVN 60  
 Qy 61 PYLGFEMGYDWLGKMAYGSDVNGAKAQGVOLTAKLGYPITDDLDIYTLLGGMWRA 120  
 Db 61 PYLGFEMGYDWLGKMAYGSDVNGAKAQGVOLTAKLGYPITDDLDIYTLLGGMWRA 120  
 Qy 61 KGNYASTGVSRSEHDTGCVSPVFAAGGVWAVTRDIATLREYQVNNGDAGTVGTRPDNGM 180  
 Db 61 KGNYASTGVSRSEHDTGCVSPVFAAGGVWAVTRDIATLREYQVNNGDAGTVGTRPDNGM 180  
 Qy 181 LS LGVSYRFQGDDAAPVVA PAPAPAPEVAKFTLKS DVLNFNKATLK PBCQQALDJQY 240  
 Db 181 LS LGVSYRFQGDDAAPVVA PAPAPAPEVAKFTLKS DVLNFNKATLK PBCQQALDJQY 240  
 Qy 181 TOLSNMDPKDGSAAVLLGTYDRIGSEAYNOQLSBRKAOVSVDYLVAKGIPAGKISARGMGE 300  
 Db 181 TOLSNMDPKDGSAAVLLGTYDRIGSEAYNOQLSBRKAOVSVDYLVAKGIPAGKISARGMGE 300  
 Qy 241 SNPVTGNTCDNYKARAALIDCLAPDRREIEVKGYKEVVTQPG 344  
 Db 241 SNPVTGNTCDNYKARAALIDCLAPDRREIEVKGYKEVVTQPG 344  
 Qy 301 TOLSNMDPKDGSAAVLLGTYDRIGSEAYNOQLSBRKAOVSVDYLVAKGIPAGKISARGMGE 300  
 Db 301 SNPVTGNTCDNYKARAALIDCLAPDRREIEVKGYKEVVTQPG 344

Qy	301	SNPVGTGNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTOPAG	344	Qy	301	SNPVGTGNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTOPAG	344
Db	301	SNPVGTGNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTOPAG	344	Db	301	SNPVGTGNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTOPAG	344
<b>RESULT 9</b>							
AAM48395	standard;	protein; 344 AA.		AAM47796	standard;	protein; 344 AA.	
ID	XX	XX		ID	XX	XX	
AC	AAM48395;			AC	XX	XX	
XX				XX			
DT	10-MAY-2002	(first entry)		DT	01-MAR-2002	(first entry)	
XX				XX			
DE	Klebsiella pneumoniae outer membrane protein, OmpA.			DE	Klebsiella pneumoniae OmpA protein.		
XX				XX			
KW	OmpA; outer membrane protein; cytosatic; cancer; tumour antigen.			KW	OmpA; enterobacterium; antibacterial; antifungal; antiviral; antiparasitic; antimicrobial; infection.		
XX				XX			
OS	Klebsiella pneumoniae.			OS	Klebsiella pneumoniae.		
XX				XX			
PN	WO200182959-A1.			PN	WO200187326-A1.		
XX				XX			
PD	08-NOV-2001.			PD	22-NOV-2001.		
XX				XX			
PR	03-MAY-2001; 2001WO-FR001348.			PR	16-MAY-2001; 2001WO-FR001490.		
XX				XX			
PR	04-MAY-2000; 2000FR-00005702.			PR	16-MAY-2000; 2000FR-00006199.		
XX				XX			
PA	(FABR ) FABRE MEDICAMENT SA PIERRE.			PA	(FABR ) FABRE MEDICAMENT SA PIERRE.		
XX				XX			
PI	Reno T, Invernizzi I, Bonnefoy J;			PI	Jeanmin P, Delneste Y, Baussant T;		
XX				XX			
DR	WPI; 2002-066490/09.			DR	WPI; 2002-055611/07.		
XX				XX			
PS	Composition, useful for treatment and prevention of cancer, also for detecting tumor antigens, comprises an outer membrane protein and tumor lysate.			PS	Use of an enterobacterium OmpA protein for prophylactic and therapeutic treatment of viral, bacterial, fungal and parasitic infections.		
XX				XX			
PS	Claim 5; Page 25-26; 32pp; French.			PS	Claim 8; Page 24-25; 33pp; French.		
XX				XX			
CC	The present invention relates to a pharmaceutical composition, comprising an Outer Membrane Protein (e.g. OmpA), associated with a lysate of autologous and/or heterologous tumour cells. The present sequence is one such OmpA from Klebsiella pneumoniae. The composition is useful for the treatment of cancers, particularly where associated with tumour antigens, and for detecting tumour antigens.			CC	The present sequence is OmpA protein from enterobacteria Klebsiella pneumoniae. OmpA protein can be used to prepare an antimicrobial pharmaceutical composition for mucosal delivery. The composition can be used for prophylactic and therapeutic treatment of viral, bacterial, fungal and parasitic infections		
CC				CC			
SQ	Sequence 344 AA;			SQ	Sequence 344 AA;		
	Query Match 100.0%; Score 1823; DB 5; Length 344;				Query Match 100.0%; Score 1823; DB 5; Length 344;		
	Best Local Similarity 100.0%; Pred. No. 1.3e-157; Mismatches 344; Conservative 0; Indels 0; Gaps 0;				Best Local Similarity 100.0%; Pred. No. 1.3e-157; Mismatches 344; Conservative 0; Indels 0; Gaps 0;		
Qy	1 MKAIKFVINAAPKDNTWYAGGKLGLWSQYHDTGFGYNGFQNNNGPTRNDQLGAGAAGFCGYVN 60			Qy	1 MKAIKFVINAAPKDNTWYAGGKLGLWSQYHDTGFGYNGFQNNNGPTRNDQLGAGAAGFCGYVN 60		
Db	1 MKAIKFVINAAPKDNTWYAGGKLGLWSQYHDTGFGYNGFQNNNGPTRNDQLGAGAAGFCGYVN 60			Db	1 MKAIKFVINAAPKDNTWYAGGKLGLWSQYHDTGFGYNGFQNNNGPTRNDQLGAGAAGFCGYVN 60		
Qy	61 PYLGFMGYDWLGRMAYKGSVNDGAPKAQGVOLTAKLGYPTTDDLDIYTLLGMWRAQS 120			Qy	61 PYLGFMGYDWLGRMAYKGSVNDGAPKAQGVOLTAKLGYPTTDDLDIYTLLGMWRAQS 120		
Db	61 PYLGFMGYDWLGRMAYKGSVNDGAPKAQGVOLTAKLGYPTTDDLDIYTLLGMWRAQS 120			Db	61 PYLGFMGYDWLGRMAYKGSVNDGAPKAQGVOLTAKLGYPTTDDLDIYTLLGMWRAQS 120		
Qy	121 KGNYASTGVSRSEHDTGYSPVFAGGVVAVTRDIATLEYQWNNNIGDAGTVTRPDNGM 180			Qy	121 KGNYASTGVSRSEHDTGYSPVFAGGVVAVTRDIATLEYQWNNNIGDAGTVTRPDNGM 180		
Db	121 KGNYASTGVSRSEHDTGYSPVFAGGVVAVTRDIATLEYQWNNNIGDAGTVTRPDNGM 180			Db	121 KGNYASTGVSRSEHDTGYSPVFAGGVVAVTRDIATLEYQWNNNIGDAGTVTRPDNGM 180		
Qy	181 LSIGVSYRFQDAAVLYVAPAPAPAEVATKHTFLKSVDLFENFKATLKPGCQQADOLY 240			Qy	181 LSIGVSYRFQDAAVLYVAPAPAPAEVATKHTFLKSVDLFENFKATLKPGCQQADOLY 240		
Db	181 LSIGVSYRFQDAAVLYVAPAPAPAEVATKHTFLKSVDLFENFKATLKPGCQQADOLY 240			Db	181 LSIGVSYRFQDAAVLYVAPAPAPAEVATKHTFLKSVDLFENFKATLKPGCQQADOLY 240		
Qy	241 TQLSNMDPKDGSAVVLYTDRIGSEAYNQQLSEKRAVSVDYLVAKSIPAGKISARGMGE 300			Qy	241 TQLSNMDPKDGSAVVLYTDRIGSEAYNQQLSEKRAVSVDYLVAKSIPAGKISARGMGE 300		
Db	241 TQLSNMDPKDGSAVVLYTDRIGSEAYNQQLSEKRAVSVDYLVAKSIPAGKISARGMGE 300			Db	241 TQLSNMDPKDGSAVVLYTDRIGSEAYNQQLSEKRAVSVDYLVAKSIPAGKISARGMGE 300		
Qy	301 SNPVGTGNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTOPAG 344			Qy	301 SNPVGTGNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTOPAG 344		

Db	301	SNPTGTNTCDNVKARAALIDCLAPDRRVIEVKGYKEVVTQPG	344		241	TOLSNMDPKDGSAAVVLGYTDIGSEAVNQLSBEKAOSVVVDYLVAKGIPAGKISARGNGE	300
<b>RESULT 11</b>							
AD100532	ID	ADI00532 standard; protein;	344 AA.		Db	241 TOLSNMDPKDGSAAVVLGYTDIGSEAVNQLSBEKAOSVVVDYLVAKGIPAGKISARGNGE	300
XX	AC	ADI00532;			Qy	301 SNPTGTNTCDNVKARAALIDCLAPDRRVIEVKGYKEVVTQPG	344
AC	XX	15-APR-2004 (First entry)			Db	301 SNPTGTNTCDNVKARAALIDCLAPDRRVIEVKGYKEVVTQPG	344
DT	XX	Klebsiella pneumoniae OmpA P40 protein.					
DB	XX	solubility; virucide; antibacterial; parasiticide; fungicide; cytostatic; vaccine; viral; bacterial; parasitic; fungal infection; cancer; gene therapy; cosmetic; major histocompatibility complex; MHC; cytotoxic T lymphocyte; CTL; OmpA; P40.					
XX	OS	Klebsiella pneumoniae.					
PN	XX	FR2842812-A1.					
PA	XX	30-JAN-2004.					
PD	XX	26-JUL-2002; 2002FR-000009526.					
PP	XX	26-JUL-2002; 2002FR-000009526.					
PR	XX	(FABR ) FABRE MEDICAMENT SA PIERRE.					
PA	XX	PI	Beck A, Corvai N, Klinguer HC, Goetsch L;				
PA	XX	PI	Beck A, Corvai N, Klinguer HC, Goetsch L;				
DR	XX	WPI; 2004-135597/14.					
XX	XX	Solubilizing hydrophobic peptides, useful e.g. in vaccines against infectious microbes or tumors, by attachment of at least three lysine residues.					
PT	XX	XX	XX				
PT	XX	XX	XX				
PT	XX	XX	XX				
PS	XX	Disclosure; SEQ ID NO 72; 65pp; French.					
CC	XX	The invention relates to a novel method for solubilising, or improving the solubility of, a peptide in aqueous medium comprising covalent attachment of at least 3 residues of Lys, in L or D form, distributed over the N and/or C termini in the form of a linear or branched chain.					
CC	XX	The invention has virucide, antibacterial, parasitic, fungicide and cytostatic activities and may be used to generate prophylactic or therapeutic vaccines or compositions for control of viral, bacterial, parasitic or fungal infections or cancers, as well as during gene therapy procedures. The peptides of the invention may also be used in cosmetic compositions. The current sequence is that of the Klebsiella pneumoniae OmpA P40 protein of the invention.					
SQ	XX	Sequence 344 AA;					
Query Match	100.0%	Score 1823; DB 8; Length 344;					
Best Local Similarity	100.0%	Pred. No. 1.3e-157;					
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Qy	1	MKAIFVLNAAPKDNTWYAGGKLGMWSQYHDTGFYGNFGQNNGPTRNDQLGAGAEGGYQVN	60		1	MKAIFVLNAAPKDNTWYAGGKLGMWSQYHDTGFYGNFGQNNGPTRNDQLGAGAEGGYQVN	60
Db	1	MKAIFVLNAAPKDNTWYAGGKLGMWSQYHDTGFYGNFGQNNGPTRNDQLGAGAEGGYQVN	60		1	MKAIFVLNAAPKDNTWYAGGKLGMWSQYHDTGFYGNFGQNNGPTRNDQLGAGAEGGYQVN	60
Qy	61	PYLGFENGYDWLGRMAYKGSDVNGAFKAQGVQLTAKLYPTDDLDIYTLLGGMWRADS	120		61	PYLGFENGYDWLGRMAYKGSDVNGAFKAQGVQLTAKLYPTDDLDIYTLLGGMWRADS	120
Db	61	PYLGFENGYDWLGRMAYKGSDVNGAFKAQGVQLTAKLYPTDDLDIYTLLGGMWRADS	120		61	PYLGFENGYDWLGRMAYKGSDVNGAFKAQGVQLTAKLYPTDDLDIYTLLGGMWRADS	120
Qy	121	KGNYASTGVSRSEHDTCGVSPVFGGYEWAVTRDIATRLXEVANNNGDAITVGTRDNGM	180		121	KGNYASTGVSRSEHDTCGVSPVFGGYEWAVTRDIATRLXEVANNNGDAITVGTRDNGM	180
Db	121	KGNYASTGVSRSEHDTCGVSPVFGGYEWAVTRDIATRLXEVANNNGDAITVGTRDNGM	180		121	KGNYASTGVSRSEHDTCGVSPVFGGYEWAVTRDIATRLXEVANNNGDAITVGTRDNGM	180
Qy	181	LSLGVSYRFQEDDAAPVYAP	240		181	LSLGVSYRFQEDDAAPVYAP	240
Db	181	LSLGVSYRFQEDDAAPVYAP	240		181	LSLGVSYRFQEDDAAPVYAP	240
Query Match	100.0%	Score 1823; DB 8; Length 344;					
Best Local Similarity	100.0%	Pred. No. 1.3e-157;					
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							

8

*S. enteritidis*, *S. panama* and *S. dublin*. A vaccine prepared using an oligosaccharide from *S. enteritidis* can be used to provide protection against septicæmia caused by *S. typhi* and against typhoid fever, as well as to protect humans and animals from toxic infections and zoonosis caused by Salmonella of the same serogroup. The carrier proteins enhance the immunogenicity of the oligo- or polysaccharide antigens, such as the Vi antigen, increases additional Salmonella capsule antigens, such as the Vi antigen, increases the vaccine's efficacy against encapsulated bacteria. The present sequence, protein LP40, is a preferred example of a carrier protein which can be used in the immunocomplex. It is obtained by recombinant expression of a modified Kleb. pneumoniae I-145 P40 gene in *E. coli*.

## Sequence 344 AA;

Query Match 99.7%; Score 1818; DB 2; Length 344;

Best Local Similarity 99.7%; Pred. No. 3. 6e-15; 0; Mismatches 1; Indels 0; Gaps 0;

XX Sequence 344 AA;

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Qy 1 MKAIFVINAAPKDNTWYAGGKGWSQYHDTGYGNGFONNNGPTRNDLQAGAAGGGYQVN 60
Db 1 MKAIFVINAAPKDNTWYAGGKGWSQYHDTGYGNGFONNNGPTRNDLQAGAAGGGYQVN 60
Qy 61 PYLGFMEMYDWLGRMAYKGSVDNGAFKAQGVLTAKGYPTIDLDIYTRLGGMWRADS 120
Db 61 PYLGFMEMYDWLGRMAYKGSVDNGAFKAQGVLTAKGYPTIDLDIYTRLGGMWRADS 120
Qy 121 KGNYASTGSRSRSEHDGTGSPVFAAGGVENAVTRDIATRLYEQWNNIGDAGTYGTRPDMG 180
Db 121 KGNYASTGSRSRSEHDGTGSPVFAAGGVENAVTRDIATRLYEQWNNIGDAGTYGTRPDMG 180
Qy 181 LSLGVSYRFQEDAAPVVAAPAPAPEVATAKHTFLSDVLENFKATLKPEQQALDLY 240
Db 181 LSLGVSYRFQEDAAPVVAAPAPAPEVATAKHTFLSDVLENFKATLKPEQQALDLY 240
Qy 241 TQLSNMDPKDGSAVVILGYTDRISSEANQNQLESEKRAQSVDYLVAKGIPAKGISARGME 300
Db 241 TQLSNMDPKDGSAVVILGYTDRISSEANQNQLESEKRAQSVDYLVAKGIPAKGISARGME 300
Qy 301 SNPVTGNTCDNVKARAALIDCLAPDRRYVEIYVKGYKEVTTOPAG 344
Db 301 SNPVTGNTCDNVKARAALIDCLAPDRRYVEIYVKGYKEVTTQPQG 344

```

RESULT 15

XX AAB67771 standard; protein: 452 AA.

AC AAB67771;

XX DT 11-JUN-2001 (First entry)

DE Outer membrane Protein A; OmpA; P40; enterobacteria; nasal composition; RSV; RSV infection; lung; respiratory tract; vaccine.

XX OS Synthetic.

OS Klebsiella pneumoniae.

OS Respiratory syncytial virus.

XX PN WO200121203-A1.

XX PD 29-MAR-2001.

XX PP 22-SEP-2000; 2000WO-FR002626.

XX PR 23-SEP-1999; 99FR-00011888.

PA (FABR ) FABRE MEDICAMENT SA PIERRE.

XX Corvaies N, Goesch L;

XX PI 2001-257929/26.

DR

DR N-PSDB; AAP80153.

Vaccine against respiratory syncytial virus, comprises enterobacterial outer membrane protein and viral immunogen, provides protective response throughout the respiratory tract.

XX Example 2; Page 31-32; 39pp; French.

The present sequence represents a fusion protein comprising a Klebsiella pneumoniae outer membrane protein A (OmpA) designated P40 and a respiratory syncytial virus (RSV) antigen. Enterobacterium OmpA proteins, associated with an immunogenic peptide from RSV are used to prepare a nasal composition that induces a protective response against RSV infection in the upper and lower (lung) respiratory tract. OmpA potentiates the immune response to some immunogenic peptides, eliminating the need for adjuvants. The method is useful for producing vaccines for prevention or treatment of RSV infections

XX SQ Sequence 452 AA;

```

Query Match 99.7%; Score 1818; DB 4; Length 452;
Best Local Similarity 99.7%; Pred. No. 5. 4e-17;
Matches 343; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy	1 MKAIFVINAAPKDNTWYAGGKGWSQYHDTGYGNGFONNNGPTRNDLQAGAAGGGYQVN 60	61 PYLGFMEMYDWLGRMAYKGSVDNGAFKAQGVLTAKGYPTIDLDIYTRLGGMWRADS 120	61 PYLGFMEMYDWLGRMAYKGSVDNGAFKAQGVLTAKGYPTIDLDIYTRLGGMWRADS 120	61 KGNYASTGSRSRSEHDGTGSPVFAAGGVENAVTRDIATRLYEQWNNIGDAGTYGTRPDMG 180	61 PYLGFMEMYDWLGRMAYKGSVDNGAFKAQGVLTAKGYPTIDLDIYTRLGGMWRADS 120	61 KGNYASTGSRSRSEHDGTGSPVFAAGGVENAVTRDIATRLYEQWNNIGDAGTYGTRPDMG 180	61 PYLGFMEMYDWLGRMAYKGSVDNGAFKAQGVLTAKGYPTIDLDIYTRLGGMWRADS 120	61 KGNYASTGSRSRSEHDGTGSPVFAAGGVENAVTRDIATRLYEQWNNIGDAGTYGTRPDMG 180	61 PYLGFMEMYDWLGRMAYKGSVDNGAFKAQGVLTAKGYPTIDLDIYTRLGGMWRADS 120
----	---	---	---	---	---	---	---	---	---

Db 1 MKAIFVINAAPKDNTWYAGGKGWSQYHDTGYGNGFONNNGPTRNDLQAGAAGGGYQVN 60

Db 1 MKAIFVINAAPKDNTWYAGGKGWSQYHDTGYGNGFONNNGPTRNDLQAGAAGGGYQVN 60

Db 121 KGNYASTGSRSRSEHDGTGSPVFAAGGVENAVTRDIATRLYEQWNNIGDAGTYGTRPDMG 180

Db 121 KGNYASTGSRSRSEHDGTGSPVFAAGGVENAVTRDIATRLYEQWNNIGDAGTYGTRPDMG 180

Db 181 LSLGVSYRFQEDAAPVVAAPAPAPEVATAKHTFLSDVLENFKATLKPEQQALDLY 240

Db 181 LSLGVSYRFQEDAAPVVAAPAPAPEVATAKHTFLSDVLENFKATLKPEQQALDLY 240

Db 181 LSLGVSYRFQEDAAPVVAAPAPAPEVATAKHTFLSDVLENFKATLKPEQQALDLY 240

Db 181 LSLGVSYRFQEDAAPVVAAPAPAPEVATAKHTFLSDVLENFKATLKPEQQALDLY 240

Db 241 TQLSNMDPKDGSAVVILGYTDRISSEANQNQLESEKRAQSVDYLVAKGIPAKGISARGME 300

Db 241 TQLSNMDPKDGSAVVILGYTDRISSEANQNQLESEKRAQSVDYLVAKGIPAKGISARGME 300

Db 301 SNPVTGNTCDNVKARAALIDCLAPDRRYVEIYVKGYKEVTTOPAG 344

Db 301 SNPVTGNTCDNVKARAALIDCLAPDRRYVEIYVKGYKEVTTQPQG 344

Qy 301 SNPVTGNTCDNVKARAALIDCLAPDRRYVEIYVKGYKEVTTQPQG 344

Db 301 SNPVTGNTCDNVKARAALIDCLAPDRRYVEIYVKGYKEVTTQPQG 344

Search completed: November 26, 2005, 00:05:49  
Job time : 192 secs

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Run on:	November 26, 2005, 00:03:28 ; Search time 46 Seconds (without alignments)
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Scoring table:	BLOSUM62
GapOpen:	10.0
GapExt:	0.5
GenCore version:	5.1.6
Copyright:	(c) 1993 - 2005 Compugen Ltd.
OM protein - protein search, using sw model	
Sequence 11012, A	US-09-189-039A-11012
Sequence 15, AppI	US-08-572-447C-15
Sequence 15, AppI	US-09-267-747-15
Sequence 11, AppI	US-08-572-447C-11
Sequence 11, AppI	US-09-267-747-11
Sequence 18046, A	US-09-229-991A-18046
Sequence 13729, A	US-09-189-039A-13729
Sequence 17612, A	US-09-252-991A-17612
Sequence 6870, Ap	US-09-328-352-6870
Sequence 29881, A	US-09-252-991A-29881
Sequence 13, AppI	US-08-572-447C-13
Sequence 13, AppI	US-09-267-747-13
Sequence 12745, A	US-09-902-540-12745
Sequence 12463, A	US-09-902-540-12463
Sequence 26245, A	US-09-252-991A-26245
Sequence 19373, A	US-09-252-991A-19373
Sequence 6621, Ap	US-09-328-352-6621
Sequence 158	8.7

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

US-09-489-039A-7451

MINIMUM MATCHES 1000

Listing first 45 summaries

Tasseled Parrotlet ~~AAA~~\*

1: /cggn2\_6/prodata/1.iaa/5\_COMB.pep:\* ; TITLE OF INVENTION : PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/489,039A  
SEARCHED AND SERIALIZED

CURRENT FILING DATE: 28888-01-27  
4: /cgn2 6:/ptodata/1/1aa/pcnus comb.prf:\*\*

PRIOR FILING DATE: 1999-01-29  
/ / / / /

Prod No : NC in the number of samples mentioned by chance to have 2  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO: 7451

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

סמסטר י

Result No.	Score	Query Match	Length	DB ID	Description
1	1782	97.8	385	2	US-0-9-489-039A-7451
2	1781	97.7	335	2	US-0-8-316-500A-2
3	1781	97.7	335	2	US-0-9-679-750-A
4	1279	70.2	384	2	US-0-9-543-681A-7922
5	984	54.0	179	2	US-0-8-336-500A-4
6	984	54.0	179	2	US-0-9-679-750-A
7	671	36.8	364	2	US-0-9-809-665A-151
8	667	36.6	364	2	US-0-9-418-980-A
9	667	36.6	364	2	US-0-9-506-078-45
10	662.5	36.3	359	1	US-0-8-457-997B-2
11	662.5	36.3	359	2	US-0-8-467-722A-2
12	662.5	36.3	359	2	US-0-9-451-184-A
13	646.5	35.5	369	2	US-0-9-809-665A-153
14	639.5	35.1	369	2	US-0-9-418-980-10
15	639.5	35.1	369	2	US-0-9-506-078-46
16	586.5	32.2	338	1	US-0-8-210-384-1
17	379	20.8	72	2	US-0-8-836-500A-6
18	379	20.8	72	2	US-0-9-679-750-A
19	281	15.4	53	2	US-0-8-336-500A-8
20	281	15.4	53	2	US-0-9-679-750-A
21	242.5	13.3	379	2	US-0-9-328-332-5219
22	231.5	12.7	351	2	US-0-9-252-991A-30094
23	224.5	12.3	349	2	US-0-9-513-610-A-2
24	200	11.0	342	2	US-0-9-002-15847
25	199	10.9	235	2	US-0-9-252-991A-1595
26	193.5	10.6	259	2	US-0-9-489-019A-14179
27	184.5	10.1	566	2	US-0-9-489-019A-14179

Query Match	Score	DB	Length	Start	End	Indels	Mismatches	Conservative	Best Local Similarity	Score	DB	Length	Start	End	Indels	Mismatches	Conservative	Best Local Similarity	
Qy																			
Ddb																			
Qy	6	VINAAPKDNTWAGKLUGWSQYHTDGFYGNNGQNNGPTRNOLGAGAAGGG	1782	DB	2				97.8%	Score	1782	DB	2						
Ddb	47	VAOAAPDNTWAGKLUGWSQYHTDGFYGNNGQNNGPTRNOLGAGAAGGG	169	DB	2				99.4%	Pred.	No.	4	3e-169	0					
Qy	66	EMGDWLGRMAYKGSVDNGAFKAQGVOLTAKLGYPTIDDD1YTRLGGMWFA	107	DB	2				EMGDWLGRMAYKGSVDNGAFKAQGVOLTAKLGYPTIDDD1YTRLGGMWFA	Score	107	DB	2						
Ddb	107	EMGDWLGRMAYKGSVDNGAFKAQGVOLTAKLGYPTIDDD1YTRLGGMWFA	107	DB	2				EMGDWLGRMAYKGSVDNGAFKAQGVOLTAKLGYPTIDDD1YTRLGGMWFA	Pred.	No.	4	3e-107	0					
Qy	126	STGVSRSHDTCVSVPAGGVWAVTRDIATLEYQVNNTGDA GTVGRPRP	107	DB	2				STGVSRSHDTCVSVPAGGVWAVTRDIATLEYQVNNTGDA GTVGRPRP	Score	126	DB	2						
Ddb	167	STGVSRSHDTCVSVPAGGVWAVTRDIATLEYQVNNTGDA GTVGRPRP	107	DB	2				STGVSRSHDTCVSVPAGGVWAVTRDIATLEYQVNNTGDA GTVGRPRP	Pred.	No.	4	3e-167	0					
Qy	186	SYRFQEDAAPIVVAAPAPAPAPVATKHTFLKS DVLNFNKATLKPEQQAL	107	DB	2				SYRFQEDAAPIVVAAPAPAPAPVATKHTFLKS DVLNFNKATLKPEQQAL	Score	186	DB	2						
Ddb	227	SYRFQEDAAPIVVAAPAPAPAPVATKHTFLKS DVLNFNKATLKPEQQAL	107	DB	2				SYRFQEDAAPIVVAAPAPAPAPVATKHTFLKS DVLNFNKATLKPEQQAL	Pred.	No.	4	3e-227	0					
Qy	246	MDPKDGSAAVLGYTDRIGSEANQNQLSEKRA SVDYLVAKC1PAGK1SARO	107	DB	2				MDPKDGSAAVLGYTDRIGSEANQNQLSEKRA SVDYLVAKC1PAGK1SARO	Score	246	DB	2						
Ddb	287	MDPKDGSAAVLGYTDRIGSEANQNQLSEKRA SVDYLVAKC1PAGK1SARO	107	DB	2				MDPKDGSAAVLGYTDRIGSEANQNQLSEKRA SVDYLVAKC1PAGK1SARO	Pred.	No.	4	3e-287	0					
Qy	306	GNTCDNYKARALIIDLCLAPDRIVEIEVKYKEVVTOPA	107	DB	2				GNTCDNYKARALIIDLCLAPDRIVEIEVKYKEVVTOPA	Score	306	DB	2						
Ddb	347	GNTCDNYKARALIIDLCLAPDRIVEIEVKYKEVVTOPA	107	DB	2				GNTCDNYKARALIIDLCLAPDRIVEIEVKYKEVVTOPA	Pred.	No.	4	3e-347	0					

ALIGNMENTS

RESULT 1

US-09-489-0139A-7451  
; Sequence 7451, Application US/09489039A  
; Patent No. 6,10836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709-2004001  
; CURRENT APPLICATION NUMBER: US/09/489-039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 7451  
; LENGTH: 385  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-0139A-7451

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**RESULT 3**  
 US-09-679-750-2 Application US/09679750  
 i Sequence 2 Application US/09679750  
 ; Patent No. 6780420  
 ; GENERAL INFORMATION:  
 APPLICANT: Banz, Hans  
 Bausant, Thierry  
 Haeuw, Jean-Francois  
 Nguyen Ngoc, Thien  
 TITLE OF INVENTION: Carrier Protein Having an Adjuvant Effect, Immunogenic Complex Containing It, Process for Their Preparation, Nucleotide Sequence and Vaccines  
 ; Patent No. 6780420  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Rockey, Milnamow & Katz, Ltd.  
 STREET: 180 N. Stateon, 2 Prudential Plaza, Suite 4700  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: U.S.A.  
 ZIP: 60601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/679,750  
 FILING DATE: 08-Oct-2000  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/836,500  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Katz, Martin L.  
 REGISTRATION NUMBER: 25,011  
 REFERENCE/DOCKET NUMBER: PIE1514P0180US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-616-5400  
 TELEFAX: 312-616-4460  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 335 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-679-750-2  
 Query Match 97.7%; Score 1781; DB 2; Length 335;  
 Best Local Similarity 100.0%; Prod. No. 4.4e-169; Mismatches 0; Indels 0; Gaps 0;  
 Matches 335; Conservative 0;  
 Qy 10 APKDNTWYAGKLGKWSQHDTGFGNGQNINNGPTRNDQDQGAGFGQYQNPYLGFEMGY 69  
 Db 1 APKDNTWYAGKLGKWSQHDTGFGNGQNINNGPTRNDQDQGAGFGQYQNPYLGFEMGY 60  
 Qy 70 DWLGRMAYKGSVDNGAKFAQGVOLTAKLGYPITDLDIYTRLGGMWRAISKGNYASTGV 129  
 Db 61 DWLGRMAYKGSVDNGAKFAQGVOLTAKLGYPITDLDIYTRLGGMWRAISKGNYASTGV 120  
 Qy 130 SRSEHDGTGVSPPVAGGVEMAVTRODIAATRLYEQWNNNIGDAGTVGTRPDNGMLSLGVSYRF 189  
 Db 121 SRSEHDGTGVSPPVAGGVEMAVTRODIAATRLYEQWNNNIGDAGTVGTRPDNGMLSLGVSYRF 180  
 Qy 190 QGDDAAPVVAAPAPAPEVATAKFTLKSVDLFNFNKATLKPEGQOALDQLYTQLSNMDPK 249  
 Db 181 QGDDAAPVVAAPAPAPEVATAKFTLKSVDLFNFNKATLKPEGQOALDQYTLQLSNMDPK 240  
 Qy 250 DGSAVVLGYTRDGGSEAQNQLSERARAQSVDLVAKGIAGKISARGMGGSNPVTGNTC 309



CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/679,750  
 FILING DATE: 08-OCT-2000  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/836,500  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Katz, Martin L.  
 REGISTRATION NUMBER: 25,011  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-616-5400  
 TELEX/FAX: 312-616-5600  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 179 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 US-09-679-750-4

Query Match 54.0%; Score 984; DB 2; Length 179;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-90; Gaps 0;  
 Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 APKONTWAGKLGWSQYHDTGFGNGFVNNGPTRNDGAGAAGGGVQNPYLGFEMGY 69  
 Db 1 APKONTWAGKLGWSQYHDTGFGNGFVNNGPTRNDGAGAAGGGVQNPYLGFEMGY 60

Qy 70 DWLGRMAYKGSVDNGAFKAQGVOLTAKLGYPITDDIYTRLGMMWRADSKCNYASTGV 129  
 Db 61 DWLGRMAYKGSVDNGAFKAQGVOLTAKLGYPITDDIYTRLGMMWRADSKCNYASTGV 120

Qy 130 SRSEHDGTGSPVFAAGGVENAVTRDIATLEYQWNNNCDAIGTYGTRPDNGMLSLGVSYR 188  
 Db 121 SRSEHDGTGSPVFAAGGVENAVTRDIATLEYQWNNNCDAIGTYGTRPDNGMLSLGVSYR 179

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RESULT 7  
 US 09-809-665A-151  
 Sequence 151, Application US/09809665A  
 PARENT NO. 679050  
 GENERAL INFORMATION:  
 APPLICANT: Lowry E., David, et al.  
 FILE REFERENCE: 28341/00435  
 CURRENT APPLICATION NUMBER: US/09/809,665A  
 CURRENT FILING DATE: 2001-03-15  
 PRIOR APPLICATION NUMBER: 60/153,453  
 PRIOR FILING DATE: 1999-09-10  
 PRIOR APPLICATION NUMBER: 60/128,689  
 PRIOR FILING DATE: 1999-04-09  
 PRIOR APPLICATION NUMBER: 09/545,199  
 PRIOR FILING DATE: 2000-04-06  
 NUMBER OF SEQ ID NOS: 197  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 151  
 LENGTH: 364  
 TYPE: PRT  
 ORGANISM: Actinobacillus pleuropneumoniae  
 US 09-809-665A-151

Query Match 36.8%; Score 671; DB 2; Length 364;  
 Best Local Similarity 42.4%; Pred. No. 2.6e-58;  
 Matches 153; Conservative 54; Mismatches 122; Indels 32; Gaps 10;

Qy 1 MKAIFVNAAPKDNTWAGKLGWSQYHDTGFGNGFVNNGPTRNDGAGAAGGGVQNPYLGFEMGY 56  
 Db 11 LSAAVAQAQPQNTFYACAKGWAESDIBQIOLDSAKNTDRGTYGINRNSVTYGVFGG 70

Qy 57 YQV-NPYLGF -EMGYDWLGRM---AYKGSVDNGAFK--AQGVOLTAKLGYPITDDLD 106  
 Db 71 YQV-NPYLGF -EMGYDWLGRM---AYKGSVDNGAFK--AQGVOLTAKLGYPITDDLD 106

Query Match 36.6%; Score 667; DB 2; Length 364;  
 Best Local Similarity 42.1%; Pred. No. 6.5e-58;  
 Matches 152; Conservative 54; Mismatches 123; Indels 32; Gaps 10;  
 SEQ ID NO: 8  
 LENGTH: 364  
 TYPE: PRT  
 ORGANISM: Actinobacillus pleuropneumoniae  
 US-09-679-750-8

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RESULT 8  
 US 09-418-980-B  
 Sequence 8, Application US/09418980  
 PARENT NO. 6713071  
 GENERAL INFORMATION:  
 APPLICANT: Campos, Manuel  
 APPLICANT: Baarsch, Mary Jo  
 APPLICANT: Rosey, Everett  
 APPLICANT: Ankenbauer, Robert  
 APPLICANT: Warren-Stewart, Lynn  
 APPLICANT: Suiter, Brian  
 APPLICANT: Keach, Robin  
 TITLE OF INVENTION: NOVEL PROTEINS FROM ACTINOBACILLUS PLEUROPNEUMONIAE  
 CURRENT APPLICATION NUMBER: US/09/418,980  
 CURRENT FILING DATE: 1999-10-14  
 NUMBER OF SEQ ID NOS: 96  
 SOFTWARE: PatentIn Ver. 2.0  
 FILE REFERENCE: PC9854A  
 SEQ ID NO: 8

Query Match 36.6%; Score 667; DB 2; Length 364;  
 Best Local Similarity 42.1%; Pred. No. 6.5e-58;  
 Matches 152; Conservative 54; Mismatches 123; Indels 32; Gaps 10;

Qy 1 MKAIFVNAAPKDNTWAGKLGWSQYHDTGFGNGFVNNGPTRNDGAGAAGGGVQNPYLGFEMGY 56  
 Db 11 LSAAVAQAQPQNTFYACAKGWAESDIBQIOLDSAKNTDRGTYGINRNSVTYGVFGG 70

Qy 57 YQV-NPYLGF -EMGYDWLGRM---AYKGSVDNGAFK--AQGVOLTAKLGYPITDDLD 106  
 Db 71 YQV-NPYLGF -EMGYDWLGRM---AYKGSVDNGAFK--AQGVOLTAKLGYPITDDLD 106

Query Match 36.6%; Score 667; DB 2; Length 364;  
 Best Local Similarity 42.4%; Pred. No. 2.6e-58;  
 Matches 153; Conservative 54; Mismatches 122; Indels 32; Gaps 10;

Qy 1 MKAIFVNAAPKDNTWAGKLGWSQYHDTGFGNGFVNNGPTRNDGAGAAGGGVQNPYLGFEMGY 56  
 Db 11 LSAAVAQAQPQNTFYACAKGWAESDIBQIOLDSAKNTDRGTYGINRNSVTYGVFGG 70

Qy 57 YQV-NPYLGF -EMGYDWLGRM---AYKGSVDNGAFK--AQGVOLTAKLGYPITDDLD 106

**RESULT 9**

US-09-056-078-45  
Sequence 45, Application US/09506078  
Patent No. 6911206  
GENERAL INFORMATION:  
APPLICANT: Pfizer Products Inc.  
TITLE OF INVENTION: FUSION PROTEINS COMPRISING CARRIERS THAT CAN INDUCE A TITLE OF INVENTION: DUAL IMMUNE RESPONSE  
FILE REFERENCE: PCJL0202A  
CURRENT APPLICATION NUMBER: US/09/506,078  
CURRENT FILING DATE: 2000-02-16  
EARLIER APPLICATION NUMBER: N/A  
EARLIER FILING DATE: 1999-02-17  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 45  
LENGTH: 364  
TYPE: PRT  
ORGANISM: *Actinobacillus pleuropneumoniae*  
US 09-206-078-45

Query Match 36.6%; Score 667; DB 2; Length 364;

Best Local Similarity 42.1%; Pred. No. 6\_5e-58;  
Matches 152; Conservative 54; Mismatches 123; Indels 32; Gaps 10;

Qy 1 MKAIIFVNLNAPKDNNTWAGKLGMSQYNTGFGYNGFQNNGPTR----NDQLGAGAFGG 56  
Db 11 LSAAAVAAQAPQQTIFYAGAKAGWASHFGIEQUDSAKNTDQTKYGINRNSVTYGFEG 70  
Qy 57 YQV--NPVLFGE - EMGYDWLGRM -- AYKGSDUNGAPK - AGQVQLTAKLGYPITDDLD 106  
Db 71 YQTLNQDKLGLAAELGYDYFGYRVSKEKGKADKKTFRAAHGATIALKPSYEVLFDL 130  
Qy 107 IYRLRG-GMWRADSKGNVASTGVSRSEIDTGVPVAGGVENAVTRDIATRLEYQVN 165  
Db 131 VYGRVGAIVLNNTYKTENDAQEVKTRRFQS - SLILGAGVETAILPPLAARVEYQMLN 188  
Qy 166 IGDA-----GTVGTRDNGMLSLGGSYRFGQEDAAPPVAPAPAPEVATKHFTLKS 217  
Db 189 AGKASYSTINRMGATDYSISVSGAUSYRFG-GAYVAAPA-----VETKNFAFS 241  
Qy 218 DVLFNPNKATLKPQGQDQLQYTLQSNMDPKDGSAVVLYGTDIGSEANQOLSEKRAQ 277  
Db 242 DVLPFAFGSKNLKPAAATAALDAMQTEINNGLSNRAIQYNGYDRIGEASNLKLSQRAE 301  
Qy 278 SVVDYLVAKGIPACKISARGMGESBNPVTGNTCDNVKAALIDCLAPDRVTEVKGYK 337  
Db 302 TVANYIVTSKGAPAANVTAVGYGEANPVGATCDKVKGKALIACLAPDRVVEQVQGTKE 361

RESULT 11

US 08-467-722A-2  
Sequence 2, Application US/08467722A  
Patent No. 6030626  
GENERAL INFORMATION:  
APPLICANT: Kolattukudy, P. E.  
TITLE OF INVENTION: Otitis Media Vaccine  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Calfee, Halter and Griswold  
STREET: Suite 1800 800 Superior Avenue  
CITY: Cleveland  
STATE: Ohio  
COUNTRY: U.S.A.  
ZIP: 44114-2688  
COMPUTER READABLE FORM:

CITY: Cleveland  
STATE: Ohio  
COUNTRY: U.S.A.  
ZIP: 44114-2688  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/457,997B  
FILING DATE: 08/08/2002  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Golrick, Mary E.  
REGISTRATION NUMBER: 34,829  
REFERENCE/DOCKET NUMBER: 2227/00102  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (216) 622-8438  
TELEFAX: (216) 241-0816  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 359 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-457-997B-2

Query Match 36.3%; Score 662.5; DB 1; Length 359;  
Best Local Similarity 43.3%; Pred. No. 1\_8e-57;  
Matches 155; Conservative 49; Mismatches 121; Indels 33; Gaps 9;

Qy 1 MKAIFVNLNAPKDNNTWAGKLGMSQYHD---TGFYGNGFQNNGPTRNDQLGAGAFGG 56  
Db 13 LAAASVAQAPQQTIFYAGAKAGWASHFGIEQUDSAKNTDQTKYGINRNSVTYGFEG 72  
Qy 57 YQV-- NPVLGFEMGYDWLGRMAYKGSVDNGAFAKQ---GVQLTAKLGYPITDDLD 108  
Db 73 YQTLNQDKLGLAAELGYDYFGYRVSKEKGKADKKTFRAAHGATIALKPSYEVLFDL 129  
Qy 109 TRIGGMWTRADSKGNYASTGV--SRSHEHTGVSPIVAGGVEMAVTRDIATRLEYQVN 165  
Db 130 GRAGVALVRSDFKFEANGTRDHKKGRTHTARASGLFAGVAYAVLPLEVRLVEYQNLTR 189  
Qy 166 IGDA-----DAGTVGTRDNGMLSLGGSYRFGQEDAAPPVAPAPAPEVATKHFTLKS 218  
Db 190 VGKYRQDKPKNTAINYPWIGCINAGSYRFQGE-APVVA---APEMVSKTFLNSD 243  
Qy 219 VLFPNPKATLKPEQGQDQLQYTLQSNMDPKDGSAVVLYGTDIGSEANQOLSEKRAQ 278  
Db 244 VTFAGFGRANLKPQAAUTDSVYGEISOV--KSRKVAVAGYTRIGSDFAVNVLQSERADS 301  
Qy 279 VVDYLVAKGIPACKISARGMGESBNPVTGNTCDNVKAALIDCLAPDRVTEVKGYK 336  
Db 302 VANYIVTSKGAPAANVTAVGYGEANPVGATCDKVKGKALIACLAPDRVVEQVQGTKE 359

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/467,722A  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Golick, Mary E.  
 REGISTRATION NUMBER: 34,329  
 REFERENCE/DOCKET NUMBER: 22727/00102  
 TELECOMMUNICATION INFORMATION:  
 TELEFAX: (216) 622-8458  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 359 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-467-722A-2

Query Match 36.3%; Score 662.5; DB 2; Length 359;  
 Best Local Similarity 43.3%; Pred. No. 1.8e-57;  
 Matches 155; Conservative 49; Mismatches 121; Indels 33; Gaps 9;

```

Qy 1 MKAIFVNLNAAPKDNTWYAGKLGMSQYHD---TGFYGNNGFQNNGPTRNDQLAGAFAFGG 56
Db 13 LAAASVAAQQAPOENTFYAGVKAGQGSFHGGINNNGAIKKGLSSSNYGRNNTFTYGVFGG 72

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Qy 57 YQV---NPYLGFEMGYDWLGRMAYKSVDNGCAFKAQ---GVQLTAKLGYPITDDLDIY 108
Db 73 YQILNQDNFLGAELGYDDEGRAKL--EAGPKKAKHTNHGAYSLKGSTEVLDGLDVY 129

Qy 109 TRLGGMWWRADSQKNASTGV---SRSEHDGTGVSPVAGGVIEWAVTRDIATLEYQMVNN 165
Db 73 YQILNQDNGLAALGYDGFGRAKLR--EAGPKKAKHTNHGAYSLKGSEYLDGLDVY 129

Qy 109 TRLGGMWWRADSQKNASTGV---SRSEHDGTGVSPVAGGVIEWAVTRDIATRLYEQMVNN 165
Db 130 GRAGVALVRSYDKFYEDANGTRDHKGRTHTARASGLFVGAYAVLPPLAVRLEYQMVTR 189

Qy 166 IG-----DAGTVGTRPDNGMLSGVSYRFQGDAAPVVAAPAPAPEAVATKHFITLKD 218
Db 190 VGYKRPQDKPNTAIPNPGICNAGISYRFQGQE-APVVA---APBMVSKTFSLNSD 243

Qy 219 VLNFNKATLKPEGQOALDQLYTOLSNMPKDSAVVLYTDIGSEANQQLSERKAQS 278
Db 244 VTFAGPKANLKPQHQATLDSVYGBISQV--KSRKVAVAGYTRIGSDAFNVKLQERADS 301

Qy 279 VVDYLWAKGIPIAGKISARGNGESNPVTGNTCDNYKARALIDCLADPDRVEIYVKYK 336
Db 302 VANFYWAKVAAADAISATGYGEANPVVTGATCDQVKRKALIACLADPDRVEIAVNGTK 359

RESULT 13  
 US-09-809-665A-153  
 Sequence 153, Application US/09809665A

PATENT NO. 670050

GENERAL INFORMATION:  
 APPLICANT: Lowery, B., David, et al.  
 TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions  
 CURRENT APPLICATION NUMBER: US/09/809,665A  
 FILE REFERENCE: 28341-04435

CURRENT FILING DATE: 2001-03-15  
 PRIORITY NUMBER: 69-115,453  
 PRIORITY FILING DATE: 1999-09-10  
 PRIORITY NUMBER: 69-128,689  
 PRIORITY FILING DATE: 1999-04-09  
 PRIORITY NUMBER: 09-545,199  
 PRIORITY FILING DATE: 2000-04-06  
 NUMBER OF SEQ ID NOS: 197  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 153  
 LENGTH: 369  
 TYPE: PRT  
 ORGANISM: Actinobacillus pleuropneumoniae

US-09-809-665A-153

Sequence 2, Application US/09451184

APPLICANT: Kolarukudy, P. E.  
 GENERAL INFORMATION:  
 PRIORITY NUMBER: 6562449  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Calfee, Halter and Griswold  
 STREET: 1400 McDonald Investment Center,  
 CITY: Cleveland  
 STATE: Ohio  
 COUNTRY: U.S.A.  
 ZIP: 44114-2688  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0

Best Local Similarity 41.1%; Pred. No. 7 46-56;  
Matches 133; Conservative 60; Mismatches 110; Indels 49; Gaps 12;

Db 183 EYQYLKAGNLNKLVRSGTQDVDFQYAPDIHSVTAGLSYRFQGAVAPVV----BPE 236

Qy 1 MKAIFVLNAPKDTWYACGKLGMSQYHTGFYG--NGFQNNNGPTRNDQ----L 49

Db 208 VATKHTFLKSDVLFNFNKATLKEGGQQLDOLYTOLSNMDPKGSAVVLYGTDRIGSAY 267

Db 11 LSAAAQAQAPQNTFYAAGKVGSSFH---HGVNQKJSGHDDRYNDRKTYGINNSV 66

Qy 237 VVTKNFAFSSDVLFDFGSSLKPAATAANGLATPAIQNGYDRIGKEAS 296

Db 268 NQOLSEKRAQSVDYLVAKGIPAKISARGMGSNPVTGNTCDNVKARAALIDCLAPDR 327

Qy 50 GAGAFGGYCV---NPYLGEMGYDWLGRMAYKGSDVNGAFK---AQGVQLTAKLGYP 100

Db 297 NLKLSQRRAETVANYLVSKGQNPAVTAVGYGEANPVTGATCDKVGRKLTACLAPDR 356

Qy 67 TYGVFGGYCQILQNQNFGLAELGYDYYCRV---RG---NDEGFRAMKHSAGLNFAKSYE 122

Db 328 VELEVKGYKEV 338

Qy 101 ITDDLDIYTRLGGMWRAKGNYASTGVSRSE---HDGVSPYFAGGYEWAVTRDIATR 157

Db 357 VEVQVQGAKNV 367

Qy 123 VLPLDLYVKVGIAVRNQDXK-KYGAENTNESTKFHKLKASTLIGAGYEALPELLAR 181

Db 358 LEYQVNNGCDACTG---GTR-----PDNGMLSLGYSYRFQEDAAPVYAPAPAP 206

Db 359 LEYQLNKAGNLNKLVRSGTQDVDFQYAPDIHSVTAGLSYRFQGAVAPVV----BPE 235

RESULT 15  
US-09-506-078-46

Qy 182 VEVQLNKAGNLNKLVRSGTQDVDFQYAPDIHSVTAGLSYRFQGAVAPVV----BPE 235

Db Sequence 46, Application US/09506078

Qy 207 EVATKHTFLKSDVLFNFNKATLKEGGQQLDOLYTOLSNMDPKGSAVVLYGTDRIGSAY 266

Db GENERAL INFORMATION:  
; APPLICANT: Pfizer Products Inc  
; PATENT NO.: 6911206  
; TITLE OF INVENTION: FUSION PROTEINS COMPRISING CARRIERS THAT CAN INDUCE A  
; DUAL IMMUNE RESPONSE  
; FILE REFERENCE: PC10202A  
; CURRENT APPLICATION NUMBER: US/09/506,078  
; CURRENT FILING DATE: 2000-02-16  
; EARLIER APPLICATION NUMBER: N/A  
; EARLIER FILING DATE: 1999-02-17  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 46  
; LENGTH: 369  
; TYPE: PRT  
; ORGANISM: Actinobacillus pleuropneumoniae  
US-09-506-078-46

Query Match 35.1%; Score 639.5; DB 2; Length 369;  
Best Local Similarity 40.7%; Prod. No. 3.7e-55; Indels 47; Gaps 11;

Db Matches 151; Conservative 60; Mismatches 113; Del 47; Gap 11;

Qy 1 MKAIFVLNAPKDTWYAGKLGMSQYHTGFYG--NGFQNNNGPTRNDQ----L 49

Db 11 LSAAAQAQAPQNTFYAAGKVGSSFH---HGVNQKLSGHDDRYNDRKTYGINNSV 66

Qy 296 NQAGFGGYQ---NPYLGEMGYDWLGRMAYKGSDVNGAFK---AOGVQLTAKLGYP 100

Db 67 TYGVFGGYCQILQNQNFGLAELGYDYYCRV---RG---NDGEFRAMKHSAGLNFAKSYE 122

Db 101 ITDDLDIYTRLGGMWRAKGNYASTGVSRSE---HDGVSPYFAGGYEWAVTRDIATR 158

Qy 50 GAGAFGGYCV---NPYLGEMGYDWLGRMAYKGSDVNGAFK---AOGVQLTAKLGYP 100

Db 123 VLPLDLYVKVGIAVRNQDXK-KYGAENTNESTKFHKLKASTLIGAGYEALPELLAR 181

Qy 159 EYQVNNGCDACTG---GTR-----PDNGMLSLGYSYRFQEDAAPVYAPAPAP 207

Db 183 EYQYLKAGNLNKLVRSGTQDVDFQYAPDIHSVTAGLSYRFQGAVAPVV----BPE 236

RESULT 14  
US-09-418-980-10

Qy Sequence 10, Application US/09418980

Db Parent No. 6713071

GENERAL INFORMATION:  
; APPLICANT: Campos, Manuel  
; APPLICANT: Baarsch, Mary Jo  
; APPLICANT: Rosey, Everett  
; APPLICANT: Ankenbauer, Robert  
; APPLICANT: Warren-Stewart, Lynn  
; APPLICANT: Suiter, Brian  
; APPLICANT: Keach, Robin  
TITLE OF INVENTION: NOVEL PROTEINS FROM ACTINOBACILLUS PLEUROPNEUMONIAE  
FILE REFERENCE: PC9154A  
CURRENT APPLICATION NUMBER: US/09/418,980  
CURRENT FILING DATE: 1999-10-14  
NUMBER OF SEQ ID NOS: 96  
SEQ ID NO: 10  
LENGTH: 369  
TYPE: PRT  
ORGANISM: Actinobacillus pleuropneumoniae  
US-09-418-980-10

Query Match 35.1%; Score 639.5; DB 2; Length 369;  
Best Local Similarity 40.7%; Pred. No. 3.7e-55;  
Matches 151; Conservative 60; Mismatches 111; Indels 47; Gaps 11;

Db 208 VATKHTFLKSDVLFNFNKATLKEGGQQLDOLYTOLSNMDPKGSAVVLYGTDRIGSAY 267

Qy 1 MKAIFVLNAPKDTWYAGKLGMSQYHTGFYG--NGFQNNNGPTRNDQ----L 49

Db 237 VVTKNFAFSSDVLFDFGSSLKPAATAANGLATPAIQNGYDRIGKEAS 296

Qy 268 NQOLSEKRAQSVDYLVAKGIPAKISARGMGSNPVTGNTCDNVKARAALIDCLAPDR 327

Db 297 NLKLSQRRAETVANYLVSKGQNPAVTAVGYGEANPVTGATCDKVGRKLTACLAPDR 356

Qy 50 GAGAFGGYCV---NPYLGEMGYDWLGRMAYKGSDVNGAFK---AQGVQLTAKLGYP 100

Db 67 TYGVFGGYCQILQNQNFGLAELGYDYYCRV---RG---NDGEFRAMKHSAGLNFAKSYE 122

Qy 101 ITDDLDIYTRLGGMWRAKGNYASTGVSRSE---HDGVSPYFAGGYEWAVTRDIATR 158

Db 123 VLPLDLYVKVGIAVRNQDXK-KYGAENTNESTKFHKLKASTLIGAGYEALPELLAR 181

Qy 159 EYQVNNGCDACTG---GTR-----PDNGMLSLGYSYRFQEDAAPVYAPAPAP 207

Search completed: November 26, 2005, 00:20:50  
Job time : 48 secs

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## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please, note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:  
  
<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

This Page Blank (uspto)

This Page Blank (uspto)

Scoring table: BLOSUM62						
Gapop 10.0 , Gapext 0.5						
Searched: 2166443 seqs, 70528306 residues						
Total number of hits satisfying chosen parameters:						
2166443						
Minimum DB seq length: 0						
Maximum DB seq length: 20000000000						
Post-processing: Minimum Match 0%						
Maximum Match 100%						
Listing first 45 summaries						
Database :						
UniProt 05.80:*						
1: uniprot_sprot:*						
2: uniprot_trembl:*						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
Result No.	Score	Query Match Length	DB ID	Description		
1	1813	99.5	344	1 OMPA_KLEPN	P24017 klebsiella	
2	1542	84.6	350	1 OMPA_ENTAE	P02935 enterobac	
3	1525.5	83.7	351	1 OMPA_SHIDY	P02935 shigella dy	
4	1513.5	83.0	347	2 O52J5K_ENTSA	Q52J5K enterobacte	
5	1511	82.9	346	1 OMPA_ECOLI	P04910 escherichia	
6	1511	82.9	346	1 OMPA_SALPA	P04910 escherichia	
7	1511	82.9	346	2 Q6PBM6_SHISO	Q6w821 shigella so	
8	1507	82.7	346	2 Q6PBM6_SHIBO	Q6pm6 shigella bo	
9	1505	82.6	346	2 Q9LJ02_ECOLI	Q91610 escherichia	
10	1501	82.3	350	2 Q5TOT3_SALCH	Q57qt3 salmonella	
11	1500	82.3	350	2 QSPD5_SALPA	Q5pgd5 salmonella	
12	1499	82.2	350	1 OMPA_SALTY	Q8Z7B0 salmonella	
13	1495	82.0	350	1 OMPA_YERPS	P02936 salmonella	
14	1487	81.6	379	2 Q8CWT6_ECOL6	Q8CWT6 escherichia	
15	1473	80.8	348	2 Q83RX2_SHIFL	Q83rx2 shigella fl	
16	1466	80.4	327	2 Q7X017_SHIFL	Q7x017 shigella fl	
17	1381.5	75.8	359	1 OMPA_SERMAG	P04845 serratia ma	
18	1364	74.8	319	2 Q6Q747_SALGL	Q6qt47 salmonella	
19	1325.5	72.7	353	1 OMPA_YERPS	Q8Z977 yersinia pe	
20	1325.5	72.7	353	1 OMPA_YERPS	P38399 yersinia ps	
21	1306	71.6	366	2 Q6DD4_BRWCT	Q6dd4 erwinia car	
22	1289	70.7	368	2 Q7N602_PHOLI	Q7n602 photorhabdu	
23	1262.5	69.3	367	2 Q9RM69_ERWCA	Q9rm69 erwinia car	
24	1128.5	61.9	238	2 Q99114_ESCVCA	Q99114 escherichia	
25	1112.5	61.0	244	2 Q47880_ESCVU	Q47880 escherichia	
26	1111	60.9	243	1 OMPA_ESCV	P24747 escherichia	
27	1110.5	60.9	244	2 Q9915_ESCVU	Q9915 escherichia	
28	1106	60.7	243	1 OMPA_ESCHE	P24754 escherichia	
29	1095.5	60.1	238	2 Q99123_ENTAB	Q99123 enterobac	
30	1089	59.7	241	1 OMPA_ESCB	Q99124 escherichia	
31	1056.5	58.0	238	1 OMPA_CITFR	P24016 citrobacter	

## ALIGNMENTS

RESULT 1						
OMPA_KLEPN						
ID	OMPA_KLEPN	STANDARD;	PRT;	344 AA.		
AC	P24017; 06435;					
DT	01-MAR-1992 (Rel. 21, Created)					
DT	15-DEC-1998 (Rel. 37, Last sequence update)					
DT	13-SEP-2005 (Rel. 48, Last annotation update)					
DE	Outer membrane protein A Precursor (Outer membrane protein II).					
GN	Name=ompA;					
OS	Klebsiella pneumoniae.					
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;					
OC	Enterobacteriaceae; Klebsiella.					
OX	NCBI_Taxid=573;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RC	STRAN=RV 308;					
RC	MEDLINE=98192544; PubMed=9524233; DOI=10.1016/S0378-1119(98)00060-2;					
RA	Nguyen T.N., Samuelson P., Sterky F., Merle-Poitte C., Robert A., Baubant T., Haeuw J.P., Uhlen M., Binz H., Stahl S.;					
RA	"Chromosomal sequencing of a PCR-based biochip capture method allowed isolation of the complete gene for the outer membrane protein A of Klebsiella pneumoniae.";					
RL	Gene 210:93-101(1998).					
[2]						
RC	STRAN=LD119;					
RX	MEDLINE=92065252; PubMed=1955870;					
RA	Lawrence J.G., Ochman H., Hartl D.L.; RT "Molecular and evolutionary relationships among enteric bacteria.";					
RT	J. Gen. Microbiol. 137:1911-1921(1991).					
RL	- - FUNCTION: Required for the action of colicins K and L and for the stabilization of mating aggregates in conjugation. Serves as a receptor for a number of T-even like phages. Also acts as a porin with low permeability that allows slow penetration of small solutes (By similarity).					
CC	- - SUBUNIT: Monomer (Probable).					
CC	- - SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.					
CC	- - SIMILARITY: Belongs to the ompA family.					
CC	- - SIMILARITY: Contains 1 OmpA-like domain.					
CC						
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is removed.					
DR	EMBL; AJ006998; CAA04501; AAA25119.1; - ; Genomic_DNA.					
DR	EMBL; P02944; 1_QJP.					
DR	HSSP; P24017; 10-195.					
DR	InterPro; IPR06664; Bac_OmpA.					
DR	InterPro; IPR02368; OmpA.					
DR	InterPro; IPR06665; OmpA_MotB.					
DR	InterPro; IPR06690; OMPA_LIKE.					



	132	SNSIAGDNHNDTGVSVPVFAGGVENVAMTRDIASTRLEYQWNINIGDAGTVGRPDNMLSVGV	191
Db	186	SYRFGQEDAAPVYAP	245
Qy	192	SYRFGQEDNAAPVYAP	251
Db	246	MDPKDGSAVVLGTYDRIGSEAYNQQLSEKRAQSVDYLVAKGTPAKITSARGMGESENPT	305
Qy	252	MDPKDGSAVVLGTYDRIGSEAYNQQLSEKRAQSVDYLVAKGTPAKITSARGMGEBSDPVT	311
Db	306	GNTCDNYKARAALJDCLAPDRRVIEIYVGKYEVTTQP	342
Qy	312	GNTCDNYKARAALJDCLAPDRRVIEIYVGKYEVTTQP	348
Db			
Qy			

RESULT 3					
	SHIDY OMP-A	SHIDY AC	STANDARD; P02975;	PRT;	351 AA.
DT	21-JUL-1986	(Ref. 01, Created) 21-JUL-1986			
DT	21-JUL-1986	(Ref. 01, Last sequence update) 13-SEP-2005			
DT	13-SEP-2005	(Ref. 48, Last annotation update)			
DB		Outer membrane protein A precursor (Outer membrane protein II).			
GN	Name=ompA;				
OS	Shigella dysenteriae.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigella				

RN [1] NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RP MEDLINE=8221414; PubMed=6283478;  
 RX Braun G.; Cole S.T.;  
 RA RT "The nucleotide sequence coding for major outer membrane protein OmpA  
 of Shigella dysenteriae.",  
 RL Nucleic Acids Res. 10:2367-2378 (1982).  
 CC -!- FUNCTION: Required for the action of colicins K and L and for the  
 CC stabilization of mating aggregates in conjugation. Serves as a  
 CC receptor for a number of T even like phages. Also acts as a porin  
 CC with low permeability that allows slow penetration of small  
 CC solutes (By similarity).  
 CC -!- SUBUNIT: Monomer (Probable).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.  
 CC -!- SIMILARITY: Belongs to the ompA family.

This Swiss-Prot entry is copyright. It is produced through a CBLM outstation - between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

DR PIR; A03435; MMEBAD.

DR HSSP: P02934; 1QJP:

UK InterPro: TPR002368 Omnia  
DR InterPro: TPR002368 Omnia

InterPro: IPR0066655; OmpA/MotB.

DR InterPro; IPR006690; OMPA-LIKE.

InterPro: IPR000498; OmpA\_tmem.

PRINTS: PRO10921; OMPADOMAIN; DR

DR PRINTS : PRO1022 ; OUTRMMBRANE.

DR ProDom; PDD000930; OmpA/MotB; 1.

DR PROSPECTIVE; DR PROSPECTIVE; DR PROSPECTIVE; DR PROSPECTIVE;

**UK** Communication: Ion translocation; Membrane: Outer membrane;

Phage recognition; Porin; Repeat; Signal; Transmembrane; Transport; ...

Outer membrane protein A.  
—  
FT CHAIN 22 351

Potential: -

TRANSMEM  
FT 55 67 Potential.

	Potential.	Potential.	Potential.	Potential.	Potential.	Potential.
FT	TRANSMEM	70	85			
FT	TRANSMEM	97	107			
FT	TRANSMEM	111	126			
FT	TRANSMEM	147	158			
FT	TRANSMEM	164	180			
FT	TRANSMEM	186	197			
FT	REPEAT	206	207	1.		
FT	REPEAT	208	209	2.		
FT	REPEAT	210	211	3.		
FT	REPEAT	212	213	4.		
FT	DOMAIN	215	243	OmpA-like.		
FT	REGION	206	213	4 x 2 AA tr.		
FT	DISULFID	316	328	By similar.		

Query Match	Score	DB 1;	Length	351;
Best Local Similarity	84.6%	Pred. No.	9, 3e-109;	
Matches	285;	Mismatches	20;	Indels
Qy	83.7%	Score 1525.5;	DB 1;	Length 351;
Db	18	VLNAAPKDNTWYAGKLGWSOYHTDGFYNGFNONNGPTRNDLGAGAFCGGYQYNPYLGF VQAQAAPKDNTWYAGKLGWSOYHTDGF1-----DNNGTENQAGAGFCGGYQYNPYVG	65	72
Qy	66	EMGYDMLGRMAKYKGSVDNGFAKAQGVQLTAKLGYPITDDLDIYTLLGGMWRADSKGNYA EMGYDMLGRMPYKGSENGAYAQAQGVQLTAKLGYPITDDLVYTRLLGGMWRADTKAHNN	125	132
Db	73	STGVSSSEBDTGVSPPFAGGVWAAITDIASTRLEYQWNINIDAGTVGTRPDNGMHLGLV VTGESEKNAHDTCVSPFAGGVWAAITDIASTRLEYQWNINIDAGHTIGTRPDNGLHLGLV	185	192
Qy	126	SYRGQEDAAPVVAAPAPAPEVATKHFTLKSDSLNFNFNKATLKPEGOALDOLYQLSN SYRGQEDAAPVVAAPAPAPEVATKHFTLKSDSLNFNFNKATLKPEGOALDOLYQLSN	245	252
Db	133	MDPKDGSAYVLLGTYDRIGSEAYNOQLSEKRAQSVDYLVAKGIPAGKISARGMGESENPT LDPKDGSVSVLLGTYDRIGSDAYNQGLSERRAQSVVDYLISKGIPADKISARGMGESENPT	305	312
Qy	186			
Db	193			
Qy	246			
Db	253			
Qy	306	GNTCDNWKARALIDCLAPDRVEIYKGKREVUTQP GNTCDNWKARALIDCLAPDRVEIYKGKREVUTQP	342	349
Db	313			

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RESULT 4					
Q52JTKS	ENTSA				
ID	Q52JTKS_ENTSA	PRELIMINARY ;	PRT ;	347 AA.	
AC	Q52JTKS;				
DT	13-SEP-2005	(TREMBLrel. 31, Created)			
DT	13-SEP-2005	(TREMBLrel. 31, Last sequence update)			
DT	13-SEP-2005	(TREMBLrel. 31, Last annotation update)			
DE	OmpA,				
GN	Name=ompA;				
OS	Enterobacter sakazakii				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales;				
OC	Enterobacteriaceae; Enterobacter.				
NCBI_TAXID	28141;				
OX	[1]				
RN		NUCLEOTIDE SEQUENCE .			
RP		STRAN=ATCC 51129;			
RC		Mohan Nair M.K., Venkitanarayanan K.S.;			
RA		"Cloning and Sequencing of the Major Outer Membrane Protein Gene ompA and Development of A Specific PCR for Rapid Detection of Enterobacter sakazakii in Infant Formula."			
RT		Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.			
RT		DRBBLI; DQ000261; AAY7984 MW. ; Genomic DNA.			
RL		SGDNITC; 347 AA. ; 37054 MW. ; RAN0148PE-200NC2 CRC564;			
DR					

Query Match 83.0%; Score 1513.5; DB 2; Length 347;  
 Best Local Similarity 84.9%; Pred. No. 7.7e-108;  
 Matches 287; Conservative 16; Mismatches 24; Indels 11; Gaps 3; Gaps 3;

6. VNAAPKDNTWYAGGKIGKGSWSOYHDGEYNGFONNNNGPTRNDQAGAGFGGYCQVNPFVGF 65

18	VAQAPKDNTWYAGKLGWSOHDGFI	-----PNDGPTHESQLGAGAFGGYQVNPNVGF	72
66	EMGYDULGRMAYKGSYVDNGAFAQGVQLTAKLGYPTDDLYTTRUGGMVRADSGKNYA	125	
73	EMGYDULGRMVKGDYTINGAFAQGVQLTAKLGYPTDDLYTTRUGGMVRADSSNNIA	132	
126	STGVRSREHDGTGVSPVAGGYEWATRDIATRLEYQVNNGDAGTVGTRPDNGMLSLGV	185	
133	G-----DDHDGTGVSPVAGGYEWATRDIATRLEYQVNNGDAGTVGTRPDNGMLSLGV	187	
186	SYRFQ-QEDAAPVVAAPAPAPAPEAVATKHFETLKSDFLNENFTATLKPEQQQLDQLTQLS	244	
188	SYRFQ-QEDAAPVVAAPAPAPAPEVOTKHFETLKSDFLNENFTATLKPEQQQLDQLTQLS	247	
245	NMDPKDGSVVUUYGTDIGSEAYNQQLSERQAQSVDYLVAKGIPACKISARGMGBNPV	304	
248	NLDPPDKGSVVNLGFTPIGSDAYNQQLSERQAQSVDYLISGIPSNKISARGMGSNPV	307	
305	TGNTCDNVKAALIDCLAPDRVEIEVKGYKEVVTQGP	342	
308	TGNTCDNVKAALIDLGDPDRVEIEVKGYKDVTQGP	345	

O15:H7 and genomic comparison with a laboratory strain K-12.";  
DNA Res. 8:11-22 (2001).  
-|- FUNCTION: Required for the action of colicins K and L and for the  
stabilization of mating aggregates in conjugation. Serves as a  
receptor for a number of T-even like phages. Also acts as a porin  
with low permeability that allows slow penetration of small  
solutes (By similarity).  
-|- SUBUNIT: Monomer (By similarity).  
-|- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane  
(By similarity).  
-|- SIMILARITY: Belongs to the *ompA* family.  
-|- SIMILARITY: Contains 1 OmpA-like domain.

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the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

Query	Match	Score	Length	DB
Best Local Similarity	84.9%	Score 1511;	DB 1;	
Matches 286;	Conservative	Pred. No. 1..2e-107;		
		Mismatches 24;	Indels 10;	Gaps 2;
Dy	6 VLNAAPKDNTWYAGGKGKLSQYHDGTGYGNQFQNNGSPTRNDQLGAGAEGGGYQVNPFYLG	65		
Db	18 VAQAAPKDNTWYTGAKLGSQYHDGTG-----NNNGPHTENQLGAGAEGGGYQVNPFYGF	72		
Dy	66 EMGYDWIGRMYAKGSVNGAFKAQGVQLTAKGYPITDDLYTRLGGMWRAIDSKGNYA	125		
Db	73 EMGYDWIGRMPYKGSVNGAFKAQGVQLTAKGYPITDDLYTRLGGMWRAIDSKGNYA	130		
SEQUENCE	346 AA; 37201 MW; 195147734CDF8B04 CRC64;			
Query Match	82.9%	Score 1511;	DB 1;	
Best Local Similarity	84.9%	Length 346;		
Matches 286;	Conservative	Pred. No. 1..2e-107;		
		Mismatches 24;	Indels 10;	Gaps 2;
Dy	6 VLNAAPKDNTWYAGGKGKLSQYHDGTGYGNQFQNNGSPTRNDQLGAGAEGGGYQVNPFYLG	65		
Db	18 VAQAAPKDNTWYTGAKLGSQYHDGTG-----NNNGPHTENQLGAGAEGGGYQVNPFYGF	72		
Dy	66 EMGYDWIGRMYAKGSVNGAFKAQGVQLTAKGYPITDDLYTRLGGMWRAIDSKGNYA	125		
Db	73 EMGYDWIGRMPYKGSVNGAFKAQGVQLTAKGYPITDDLYTRLGGMWRAIDSKGNYA	130		
SEQUENCE	346 AA; 37201 MW; 195147734CDF8B04 CRC64;			
Query Match	82.9%	Score 1511;	DB 1;	
Best Local Similarity	84.9%	Length 346;		
Matches 286;	Conservative	Pred. No. 1..2e-107;		
		Mismatches 24;	Indels 10;	Gaps 2;
Dy	126 STGVSRSEBDTGVSPVAGGVWAVTRDIATRLEYQVNINJGDAGTVTRPDNCMLSLGV	185		
Db	131 ---VYGNKHDTGVSPVAGGVWAVTRDIATRLEYQVNINJGDAGTVTRPDNCMLSLGV	187		
Dy	186 SYRFQGQEAAPVAP	245		
Db	188 SYRFQGQEAAPVAP	247		
SEQUENCE	246 MDPDGSAVVLGTYDTRGSEAYNQQLSEKRAQSVDVLVAKGIPAKGISARGMGESENPTV	305		

Db	248	LDPKDGSVVVLGYTDRIGSDAYNQGLSERRAQSVDYLKGTPADKTSARGMGESENPT	307	
Qy	306	GNTCDVNKRKAALIDCLAPDRRVTEVKRKYKEVVTQF	342	"Comparing the predicted and observed properties of proteins encoded in the genome of <i>Escherichia coli</i> K-12.";
Db	308	GNTCDVNKRKAALIDCLAPDRRVTEVKRKYKEVVTQF	344	Electrophoresis 18:1259-1313 (1997).
				[7]
RESULT 6				
OMPA_ECOLI		STANDARD; PRT; 346 AA.		
ID	OMP_ECOLI	STANDARD;	PRT;	
AC	POA910; P02924;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Outer membrane protein A precursor (Outer membrane protein III).			
DE	Name=ompA; Synonyms=con, tolg, tut; OrderedLocusName=b0957;			
CDS	Escherichia coli.			
OC	Bacteriophage; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID=562;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=K12;			
RX	MEDLINE=81053729; PubMed=6253901;			
RA	Beck E.; Bremer E.;			
RT	"Nucleotide sequence of the gene <i>ompA</i> coding the outer membrane protein II of <i>Escherichia coli</i> K-12.";			
RL	Nucleic Acids Res. 8:3011-3024(1980);			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=K12;			
RX	MEDLINE=81170587; PubMed=6260961;			
RA	Morva N.R., Nakamura K., Inouye M.;			
RT	"Gene structure of the OmpA Protein, a major surface protein of <i>Escherichia coli</i> required for cell-cell interaction.";			
RL	J. Mol. Biol. 143:317-328 (1980).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=K12;			
RX	MEDLINE=97061202; PubMed=8905232;			
RA	Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,			
RA	Kajihara M., Kanai K., Kashimoto K.,			
RA	Ikemoto K., Inada T., Itoh T., Kajihara M., Makino K., Mizobuchi K.,			
RA	Kimura S., Kitagawa M., Makino S., Masuda S., Mikitani T., Mizobuchi K.,			
RA	Mori H., Motomura K., Nakamura Y., Nishio Y., Saito N.,			
RA	Sanpei K., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,			
RA	Yano M., Horuchi T.,			
RT	A 718-rb DNA sequence of the <i>Escherichia coli</i> K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.;"			
RL	DNA Res. 3:137-155(1996).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=K12 / MG1655;			
RX	MEDLINE=9742617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;			
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,			
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,			
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			
RA	Mau B., Shao Y.;			
RT	"The complete genome sequence of <i>Escherichia coli</i> K-12."			
RL	Science 277:1453-1474 (1997).			
RN	[5]			
RP	PROTEIN SEQUENCE OF 22-346.			
RC	STRAIN=K12;			
RX	MEDLINE=81054820; PubMed=7001461;			
RA	Chen R., Schmidmayr W., Kramer C., Chen-Schmeisser U., Henning U.;			
RT	"Primary structure of major outer membrane protein II (ompA protein) of <i>Escherichia coli</i> K-12."			
RL	Proc. Natl. Acad. Sci. U.S.A. 77:4592-4596 (1990).			
RN	[6]			
RP	PROTEIN SEQUENCE OF 22-34.			
RC	STRAIN=K12 / EMG2;			
RX	MEDLINE=97443975; PubMed=9238646;			
RA	Link A.J., Robison K., Church G.M.;			
RA	"High-resolution structure of the OmpA membrane domain."			
RT	"High-resolution structure of the OmpA membrane domain."			

RL	J. Mol. Biol.	298:273-282 (2000).	Qy	66 EMGYDILGRMAYKGSVNDNGAFAKGQVOLTAKLGYPIDDDIYTRLGGMVRADSKGNYA 125
RN	[117]		Db	73 EMGYDWLGRMYPKGSTENGAYKAQGQVOLTAKLGYPIDDDIYTRLGGMVRADTSKN-- 130
RP	STRUCTURE BY NMR OF 22-197;		Qy	126 STEVRSSEBDTGVSPFAGGVWAVTRDIATRLEYQVNNGDAGTVGTRPDNGMLSLGV 185
RX	PubMed=11276554; DOI=10.1038/86214;		Db	131 --VYGRHDTGVSPFAGGVYAITPEIAIRLEYQVNNGCDAHTGTRPDNGMLSLGV 187
RA	Arora A., Abildgaard F., Bushwell J.H., Tamm L.K.;		Qy	186 SYRFQGDAAPVVAAPAPAPAEVATKHTFLJNSVLJENFKATLKPECGOALDOLYTOLSN 245
RT	"Structure of outer membrane protein A transmembrane domain by NMR spectroscopy.";		Db	188 SYRFQGDAAPVVAAPAPAPAEVATKHTFLJNSVLJENFKATLKPECGOALDOLYSQSN 247
RL	Nat. Struct. Biol. 8:334-338 (2001).		Qy	246 MDPKDGSAVVLGTYDRIGSEANQLSBKRASQVVDYLVAKGIPAKGKSARGMGEENPVT 305
RP	MASS SPECTROMETRY;		Db	248 LDPKDGSVVVLGTYDRIGSDAYNQLSERBASQVVDYLISKGTPAKGKSARGMGEENPVT 307
RX	MEDLINE=0222357; PubMed=10757971; DOI=10.1021/bi000150m;		Qy	306 GNTCDNVYKARAALIDCLAPDRREVEEVKGKEVVTQP 342
RA	Le Courte J., Whitelegge J.P., Gross A., Turk E., Wight E.M.,		Db	308 GNTCDNVKQRALIDCLAPDRREVEEVKGKIDVVTQP 344
RA	Kaback H.R., Pauli K.F.;			
RT	"Proteomics on full-length membrane proteins using mass spectrometry";			
RT	Biochemistry 39:4237-4242 (2000).			
CC	-I- FUNCTION: Required for the action of colicins K and L and for the stabilization of mating aggregates in conjugation. Serves as a receptor for a number of T-even like phages. Also acts as a porin with low permeability that allows slow penetration of small solutes.			
CC	-I- SUBUNIT: Monomer (Probable).			
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.			
CC	-I- MASS SPECTROMETRY: MW=35177; METHOD=Electrospray; RANGE=22-346; NOTE=Ref.18.			
CC	-I- SIMILARITY: Belongs to the OmpA family.			
CC	-I- SIMILARITY: Contains 1 OmpA-like domain.			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.			
CC	-I- PROTEIN: CAA3588_1; Genomic_DNA.			
DR	EMBL; D0733; BAA5715_1; -; Genomic_DNA.			
DR	EMBL; D0734; BAA5722_1; -; Genomic_DNA.			
DR	PIR; AAC0096; AAC043_1; -; Genomic_DNA.			
DR	PTR; A9707; MMDBCA.			
DR	PDB; 1BKW; X-ray; A=22-192.			
DR	PDB; 1G0; NMR; A=22-197.			
DR	PDB; 1QIP; X-ray; A=22-192.			
DR	SWISS-2DPAGE; P0A910; COLI.			
DR	ECHOBASE; P04_5; 6TH EDITION.			
DR	ECODDBASE; P028_0; 6TH EDITION.			
DR	ECODDBASE; P033_0; 6TH EDITION.			
DR	EchoBASE; EB033_1; 6TH EDITION.			
DR	EcoGene; EG10669; OmpA.			
DR	InterPro; IPR00664; Bac_OmpA.			
DR	InterPro; IPR00238; OmpA.			
DR	InterPro; IPR00665; OmpA/MotB.			
DR	InterPro; IPR00048; OmpA_LIKE.			
DR	Pfam; PF00691; OmpA_1.			
DR	PRINTS; PR01021; OMPADOMAIN.			
DR	PRINTS; PR01022; OUTRIMBRANE.			
DR	PROSITE; PS00030; OmpA/MotB_1.			
DR	PROSITE; PS01068; OmpA_1.			
DR	PROSITE; PS01068; OmpA_1.			
DR	KW Signal.			
FT	SIGNAL 1 21 Potential.			
SQ	SEQUENCE 346 AA; 37201 MW; 195147734CDF8B04 CRC64;			
Query Match	82.9%; Score 1511; DB 1; Length 346;			
Best Local Similarity	84.9%; Pred. No. 1.2e-107;			
Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;	Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;			
KW Direct protein sequencing; Ion channel; Conjugation;				
KW Phage recognition; Porin; Repeat; Signal; Transmembrane; Transport.				
Qy	6 VLNAAPKDNWYAGGKLGMSQYHDTGFYGNFGQNNGPTRNQLGAGAFGGYQVNPLGF 65			
Db	18 VAQAAPKDNWYTAKLGSQYHDTGFYQNNGPTHENOLGAGAFGGYQVNPLGF 72			
Query Match	82.9%; Score 1511; DB 1; Length 346;			
Best Local Similarity	84.9%; Pred. No. 1.2e-107;			
Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;	Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;			
Qy	6 VLNAAPKDNWYAGGKLGMSQYHDTGFYGNFGQNNGPTRNQLGAGAFGGYQVNPLGF 65			
Db	18 VAQAAPKDNWYTAKLGSQYHDTGFYQNNGPTHENOLGAGAFGGYQVNPLGF 72			
Qy	66 EMGYDILGRMAYKGSVNDNGAFAKGQVOLTAKLGYPIDDDIYTRLGGMVRADSKGNYA 125			
Db	18 VAQAAPKDNWYTAKLGSQYHDTGFYQNNGPTHENOLGAGAFGGYQVNPLGF 72			
Qy	66 EMGYDILGRMAYKGSVNDNGAFAKGQVOLTAKLGYPIDDDIYTRLGGMVRADSKGNYA 125			
Db	18 VAQAAPKDNWYTAKLGSQYHDTGFYQNNGPTHENOLGAGAFGGYQVNPLGF 72			

Qy	126	STGVRSRSEHDGTGSPVFAAGGVENAVTRDIATRLEYQWNNINGDAGTVGRPDNGMLSLGV	185	Db	131	---VYGNKHDTGVSPVFAAGGVYAITPEIATRLEYQWNNINGDAHTIGTRPDNGMLSLGV	187			
Db	131	--VYGNKHDTGTGSPVFAAGGVTAITPEIATRLEYQWNNINGDAHTIGTRPDNGMLSLGV	187	Qy	186	SYRFQQDAAPVVAAPAPAPEVATKHFILKSDVLFNFKATLKPEGQALDLYTQLSN	245			
Qy	186	SYRFQQDAAPVVAAPAPAPEVATKHFILKSDVLFNFKATLKPEGQALDLYTQLSN	245	Db	188	SYRFQQDAAPVVAAPAPAPEVATKHFILKSDVLFNFKATLKPEGQALDLYTQLSN	247			
Db	188	SYRFQQDAAPVVAAPAPAPEVATKHFILKSDVLFNFKATLKPEGQALDLYTQLSN	247	Qy	246	MDPKDGSAVVLYGTDRIGSEATNQOLSEKRAQSVDYLVAKGTPAGKTSARGMGESENPT	305			
Qy	246	MDPKDGSAVVLYGTDRIGSEATNQOLSEKRAQSVDYLVAKGTPAGKTSARGMGESENPT	305	Db	248	LDPKDGSVVLGTYTDRIGSDAYNGLSERRAQSVDYLISKGPVDKTSARGMGESENPT	307			
Db	248	LDPKDGSVVLGTYTDRIGSDAYNGLSERRAQSVDYLISKGPVDKTSARGMGESENPT	307	Qy	306	GNTCDNVKARAALIDCLADPDRVEIEVKYKEVVTQP	342			
Qy	306	GNTCDNVKARAALIDCLADPDRVEIEVKYKEVVTQP	342	Db	308	GNTCDNVKORAALIDCLADPDRVEIEVKYKEVVTQP	344			
Db	308	GNTCDNVKORAALIDCLADPDRVEIEVKYKEVVTQP	344	RESULT 9						
Q9L6J0_ECOLI										
ID	Q9L6J0	ECOLI PRELIMINARY;	PRT;	346 AA.	AC	Q9L6J0;				
AC	Q9L6J0;				DT	01-OCT-2000 (TREMBLrel. 15, Created)				
DT	05-JUL-2004 (TREMBLrel. 27, Created)				DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)				
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)				DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)				DE	Outer membrane protein A.				
DN	Name=ompA;				GN					
DN	Outer membrane protein A precursor.				OS	Escherichia coli.				
OS	Name=ompA;				OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;				
OC	Shigella boydii.				OC	Enterobacteriaceae; Escherichia.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;				OX	NCBI_TaxID=562;				
OC	Enterobacteriaceae; Shigella.				RN	[1]				
OX	NCBI_TaxID=621;				RP	NUCLEOTIDE SEQUENCE.				
RN					RC	STRAIN_RS218;				
RC	NUCLEOTIDE SEQUENCE.				DR	EMBL: AF23269; AAC371887.1; -; Genomic_DNA.				
RC	STRAIN=MalaysiaB31;				DR	HSSP; P02934; 1QP.				
RA	NIK Noorlina Shakira M.S., Kiranpal Kaur B.S., Ravichandran M., Asma I., Mohd Zaki S.,				DR	SMR; Q9L6J0; 22-197.				
RA	"Shigella boydii outer membrane protein A precursor (ompA) gene."				DR	GO: GO-0016021; C:integral to membrane; IEA.				
RA	Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.				DR	GO; GO-0093279; C:outer membrane (sensu Gram-negative Bacteria); IEA.				
RA	EMBL: AY590298; AAC02227.1; -; Genomic_DNA.				DR	GO; GO-0005198; F:structural molecule activity; IEA.				
SNR	Q6NNM6; 22-197.				DR	InterPro; IPR006664; Bac_OmpA.				
DR	GO: GO-16021; C:integral to membrane; IEA.				DR	InterPro; IPR006664; Mot_V.				
DR	DR; GO: GO-009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.				DR	InterPro; IPR020135; OmpA.				
DR	DR; GO: GO-005198; F:structural molecule activity; IEA.				DR	InterPro; IPR02368; OmpA.				
DR	DR; InterPro; IPR006664; Bac_OmpA.				DR	InterPro; IPR006665; OmpA/MotB.				
DR	DR; InterPro; IPR00235; Mot_V.				DR	InterPro; IPR006690; OmpA_LIKE.				
DR	DR; InterPro; IPR006665; OmpA/MotB.				DR	InterPro; IPR00498; OmpA_tmem.				
DR	DR; InterPro; IPR006690; OMPA_LIKE.				DR	Pfam; PF00651; OmpA; 1.				
DR	DR; InterPro; IPR000498; OmpA_tmem.				DR	Pfam; PF01389; OmpA membrane; 1.				
DR	PFAM; PF01389; OmpA; 1.				DR	PRINTS; PRO1023; NAFLGMOTY.				
DR	PRINTS; PRO1022; OMPADOMAIN.				DR	PRINTS; PRO1021; OMPADOMAIN.				
DR	PRODom; PD000930; OMPA/MotB.				DR	PRINTS; PRO1022; OUTMMBRANE.				
DR	PROSITE; PS01068; OMPA; 1.				DR	PRODom; PD000930; OMPA/MotB; 1.				
DR	PROSITE; PS01021; OMPADOMAIN.				DR	PROSITE; PS01068; OMPA; 1.				
DR	PROSITE; PS01022; OMPA/MotB; 1.				SQ	SEQUENCE 346 AA.; 37188 MW;				
DR	PROSITE; PS01068; OMPA; 1.				SQ	5736077E41BD84C3 CRC64;				
KW	SIGNAL	1	21	Potential.	Query Match 82.6%; Score 1505; DB 2; Length 346;					
FT	SEQUENCE	346 AA.	37229 MW;	E94650734CDF9239 CRC64;	Best Local Similarity 84.3%; Pred. No. 3.4e-107; Matches 284; Conservative 18; Mismatches 25; Indels 10; Gaps 2;					
SQ	SEQUENCE	346 AA.	37229 MW;	E94650734CDF9239 CRC64;	Qy	6 VLNAAPKDTNTWYAGKLGWSQYHDTGYNGFQNNNGPTRDQLGAGAFGGYQVNPNYLGF	65			
Query Match	6	Score 1507; DB 2;	Length 346;	Db	18 VAQAAPKDTNTWYTGAKLGWSQYHDTGPI-----NNNGPTHENOLGAGAFGGYQVNPNYVG	72				
Best Local Similarity	82.7%	Pred. No. 2.4e-107;	Mismatches 285; Conservative 17; Mismatches 25; Indels 10; Gaps 2;	Qy	73 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Db	73 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Qy	76 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Db	76 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Qy	77 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Db	77 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Qy	78 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Db	78 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Qy	79 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Db	79 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Qy	80 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Db	80 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Qy	81 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Db	81 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Qy	82 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Db	82 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Qy	83 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Db	83 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Qy	84 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Db	84 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Qy	85 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Db	85 EMGYDWLGRMAYKGSVNDGAFKQGVQLTAKGYPIDDDTYTRLGMMWRAKSGNYA	125				
Matches	84.6%			Qy	86 SYRFQQDAAPVVAAPAPAPEVATKHFILKSDVLFNFKATLKPEGQALDLYTQLSN	245				
Matches	84.6%			Db	86 SYRFQQDAAPVVAAPAPAPEVATKHFILKSDVLFNFKATLKPEGQALDLYTQLSN	247				

Qy	246	MDPKDGSAYVVLGTYDRIGSEAYNQOLSERKQAQSVDYLVAKGIPAGKISARGMGESENPT	305	GN Name=ompA; OrderedLocusNames=SPA1780;
Db	248	LDPKDGSVVVLGTYDRIGSDAYNQLSERKQAQSVDYLISKGIPADKISARGMGESENPT	307	OS Salmonella paratyphi-a.
Qy	306	GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEYVTTQ	342	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Db	308	GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEYVTTQ	344	OC Enterobacteriaceae; Salmonella.
				[1] _RN [1] _
				NCBI_TaxID=54388;
				NUCLEOTIDE SEQUENCE
				STRAIN=ATCC 9150;
				RX PubMed=1551982; DOI=10.1038/ng1470;
				RX McClelland M., Sanderson K.E., Clifton S.W., Latreille P., McLellan M., Porwollik S., Sabo A., Meyer R., Bieri T., Oersky P., Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G., Kohlberg S., Strong C., Du F., Carter J., Krenzki C., Layman D., Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P., Delehaty K., Fronick C., Magrin V., Nhan M., Warren W., Florea L., Spieth J., Wilson R.K.; "Comparison of genome degradation in <i>Paratyphi A</i> and <i>Typhi</i> , human-restricted serovars of <i>Salmonella enterica</i> that cause typhoid."; Nat. Genet. 36:1268-1274 (2004); DR EMBL; CP000026; AAV771696.1; -; Genomic_DNA.
				DR SMR; Q5PGD5; 22-201
				DR GO; GO:0016121; C:integral to membrane; IEA.
				DR GO; GO:0005279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
				DR GO; GO:0005198; F:structural molecule activity; IEA.
				DR InterPro; IPR01035; MotY.
				DR InterPro; IPR02368; OmpA.
				DR InterPro; IPR00665; OmpA/MotB.
				DR InterPro; IPR00690; OMPA_LIKE.
				RT The genome sequence of <i>Salmonella enterica</i> serovar Choleraesuis, a highly invasive and resistant zoonotic pathogen.";
				RT Purative hydrogenase membrane component.
				DE Name=ompA; OrderedLocusName=SC1022; Outer membrane protein.
				GN OS <i>Salmonella choleraesuis</i> ; <i>Salmonella enterica</i> ; <i>Bacteria</i> ; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; <i>Salmonella</i> .
				[1] _NCBI_TaxID=51;
				RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
				RA PubMed=5781495;
				RA Chiu C.H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y., Wang H.-S., Lee Y.-S.; "The genome sequence of <i>Salmonella enterica</i> serovar Choleraesuis, a highly invasive and resistant zoonotic pathogen.";
				RT EMBL: AB017220; AX64928.1; -; Genomic_DNA.
				DR Complete proteome; ARX64928.1; -; Genomic_DNA.
				KW KW PROSITE; PS01068; OMFA; 1.
				DR PRODOM; PP000930; OMDA/MCDB; 1.
				DR PROSITE; Ps01068; OMFA; 1.
				KW Complete proteome; ARX64928.1; -; Genomic_DNA.
				DR PRINTS; PR01023; NAFFGMOTY.
				DR PRINTS; PR01021; OMPADOMAIN.
				DR PRINTS; PR01022; OUTRMMBANE.
				DR PRODOM; PP000930; OMDA/MCDB; 1.
				DR PROSITE; Ps01068; OMFA; 1.
				KW Complete proteome; ARX64928.1; -; Genomic_DNA.
				DR SEQENCE 350 AA; 37491 MW; 7C3529A442B234FC CRC64;
				Query Match Score 1501; DB 2; Length 350;
Qy	6	VLNAAPKONTWYAGKLGMSQYHDTGFYNGFQNNNGPRTNDLGAAGFGGYQVNPNYLF	65	Best Local Similarity 83.1%; Pred. No. 8.5e-107; Length 350;
Db	18	VAQAAPKONTWYAGKLGMSQYHDTGFI---NNDPHENOLGAGAAGGGQVNPNYFG	72	Matches 280; Conservative 25; Mismatches 26; Indels 6; Gaps 2;
Qy	66	EMGYDWLGRMAYKGSKVNDNGAFAKQAGVQLTAKLGYPITDDLYTRUGGMWFRADSKNYA	125	Query Match Score 1501; DB 2; Length 350;
Db	73	EMGYDWLGRMAYKGDNINGAKYQAGVQLTAKLGYPITDDLYTRUGGMWFRADTKSNVP	132	Best Local Similarity 83.1%; Pred. No. 8.5e-107; Length 350;
Qy	126	STGVYSRSBEDGTGVSPPVFAAGGVENAVTRDIAATRLEYQVNINIGDAGTVTRPDNGMISLGV	185	Matches 280; Conservative 25; Mismatches 26; Indels 6; Gaps 2;
Db	133	G-GPSTKDDGTGSPVPPVAGIEPAITPEATRLEYQVNINIGDANTIGTRPGLLISVGV	191	Qy 6 VLNAAPKONTWYAGKLGMSQYHDTGFYNGFQNNNGPRTNDLGAAGFGGYQVNPNYLF 65
Qy	186	SYRGQEDAAVVAAPAPAPEVATKHTTLKSDVLFNPKNATURKPEGQALDQLYTOLSN	245	Db 18 VAQAAPKONTWYAGKLGMSQYHDTGFI---NNDPHENOLGAGAAGGGQVNPNYFG 72
Db	192	SYRGQQEAVVVAAPAPAPEVATKHTTLKSDVLFNPKNATURKPEGQALDQLYSOLSN	251	Qy 66 EMGYDWLGRMAYKGSKVNDNGAFAKQAGVQLTAKLGYPITDDLYTRUGGMWFRADSKNYA 125
Qy	246	MDPKDGSAYVVLGTYDRIGSEAYNQOLSERKQAQSVDYLVAKGIPAGKISARGMGESENPT	305	Db 73 EMGYDWLGRMAYKGDNINGAKYQAGVQLTAKLGYPITDDLYTRUGGMWFRADTKSNVP
Db	252	LDPKDGSVVVLGTYDRIGSDAYNQLSERKQAQSVDYLISKGIPADKISARGMGESENPT	311	Qy 126 STGVYSRSBEDGTGVSPPVFAAGGVENAVTRDIAATRLEYQVNINIGDAGTVTRPDNGMISLGV 185
Qy	306	GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEYVTTQ	342	Db 192 SYRGQEDAAVVAAPAPAPEVATKHTTLKSDVLFNPKNATURKPEGQALDQLYTOLSN 245
Db	312	GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEYVTTQ	348	Qy 246 MDPKDGSAYVVLGTYDRIGSEAYNQOLSERKQAQSVDYLVAKGIPAGKISARGMGESENPT 305
				Db 252 LDPKDGSVVVLGTYDRIGSDAYNQLSERKQAQSVDYLISKGIPADKISARGMGESENPT 311
				Qy 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEYVTTQ 342
				Db 312 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEYVTTQ 348
				RESULT 11
				Q5PGD5_SALPA PRELIMINARY;
				ID Q5PGD5;
				AC Q5PGD5;
				DT 01-FEB-2005 (TREMBrel. 29, Created)
				DT 01-FEB-2005 (TREMBrel. 29, Last sequence update)
				DT 01-FEB-2005 (TREMBrel. 29, Last annotation update)
				DE Outer membrane protein A.

RESULTS  
 RESULT 12  
 OMPA\_SALTI ID\_OMPA\_SALTI STANDARD; AC Q8Z750; Q7C962;  
 Q8Z750; Q7C962;  
 PRT; 350 AA.

RESULTS  
 RESULT 12  
 OMPA\_SALTI ID\_OMPA\_SALTI STANDARD; AC Q8Z750; Q7C962;  
 Q8Z750; Q7C962;

DT	13-SEP-2005 (Rel. 48, Created)					
DT	13-SEP-2005 (Rel. 48, Last sequence update)					
DT	13-SEP-2005 (Rel. 48, Last annotation update)					
DE	Outer membrane protein A precursor.					
GN	Name=ompA; OrderedLocusName=STY1091; t1850;					
OS	Salmonella typhi.					
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;					
OC	Enterobacteriaceae; Salmonella.					
NCB_TaxID=601;						
RN	[1]					
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].					
STRAIN=CT18;						
RC	MEDLINE=21534947; Pubmed=11677608; DOI=10.1038/35101607;					
RX	Parkhill J., Dougan G., James K.D., Pickard D., Wain J., Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Hague A., Hien T.T., Holroyd S., Jagele K., Krogh A., Larsen T.S., Leather S., Moulie S., O'Gara P., Parry C., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Rutledge B.G.; "Complete genome sequence of a multiple drug resistant <i>Salmonella enterica</i> serovar Typhi CT18."; <i>Nature</i> 413:848-852 (2001).					
RN	[2]					
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].					
STRAIN=Ty2 / ATCC 700931;						
RC	MEDLINE=21531367; Pubmed=12644504;					
RX	DOI=10.1128/JB.185.7.2330-2337.2003;					
RA	Deng W., Liou S.-F., Plunkett G. III., Mayhew G.F., Rose D.J., Burland V., Kodovianni V., Schwartz D.C., Blattner F.R.; "Comparative genomics of <i>Salmonella enterica</i> serovar Typhi strains Ty2 and CT18."; <i>J. Bacteriol.</i> 185:2330-2337 (2003).					
CC	-I - FUNCTION: Required for the action of colicins K and L and for the stabilization of mating aggregates in conjugation. Serves as a receptor for a number of T-even like phages. Also acts as a porin with low permeability that allows slow penetration of small solutes (By similarity).					
CC	-I - SUBUNIT: Monomer (probable).					
CC	-I - SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.					
CC	-I - SIMILARITY: Belongs to the ompA family.					
CC	-I - SIMILARITY: Contains 1 CmpA-like domain.					
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.					
DR	EMBL; AL016840; CD08196.1; -; Genomic DNA.					
DR	HSSP; P02934; 1QJP.					
DR	Q8ZTS0; 22-201.					
DR	IPR006664; Bac_OmpA.					
DR	InterPro; IPR0023168; OmpA.					
DR	InterPro; IPR006665; OmpA/MotB.					
DR	InterPro; IPR006650; OMPA_LIKE.					
DR	InterPro; IPR000498; OmpA.					
DR	PRINTS; PRO1021; CMFDA DOMAIN.					
DR	PRINTS; PRO1022; OUTRMBRANE.					
DR	ProDom; PD000930; OmpA/MotC; 1.					
DR	PROSITE; PS01068; OMPA_1; 1.					
DR	PROSITE; PS51123; OMPA_2; 1.					
KW	Complete proteome; Conjugation; Ion transport; Membrane; Outer membrane; Phage recognition; Porin; Transport; Signal; Transmembrane; Transport.					
FT	SIGNAL 1 21 By similarity.					
FT	CHAIN 22 350 Outer membrane protein A.					
FT	TRANSMEM 27 40 Potential.					
FT	TRANSMEM 55 67 Potential.					
Query Match	6 VLNAPKDNTWAGKLGMSQYHDTGFYNGQFQNNNGPTRNDOLGAGAFGGYQVNQVPLGF 65					
Best Local Similarity	82.2% Score 1499; DB 1; Length 350;					
Matches	279; Conservative 26; Mismatches 26; Indels 6; Gaps 2;					
SEQUENCE	350 AA; 3747 MW; EBB90059DFCAFDF3 CRC64;					
Qy	6 VLNAPKDNTWAGKLGMSQYHDTGFYNGQFQNNNGPTRNDOLGAGAFGGYQVNQVPLGF 65					
Db	18 VAQAPKDNTWAGAKLGMSQYHDTGFYQVNQVPLGF 72					
Qy	66 EMGYDWLGRMAYKGSVNDNGFAKAQGVQVLTAKLGYPITDLDLYTRLGVMWRADSKGNYA 125					
Db	73 EMGYDWLGRMYPKGDNTNGAYKAQGVQVLTAKLGYPITDLDLYTRLGVMWRADTKSNVP 132					
Qy	126 STGVSRSRSHDGTGIVSPVFGGVEWAVTRDIALEYQVNQVPLGFYTRDPDNGMLSLGV 185					
Db	133 G-GASTKDHDGTGIVSPVFGGIEAVTPPIATRLEYQVNQVPLGFYTRDPDGLSVCV 191					
Qy	186 SYRFQDQEDAPIVAPAPAPAEVATRFLKSDVLFNPNKSTLKEPGQALDLYTQLSN 245					
Db	192 SYRFQDQEAAPVVAAPAPAPAEVOTKIFTLKSDVLFNPNKSTLKEPGQALDLYTQLSN 251					
Qy	246 MDPKDGSAVVLGTYTRIGSEAYNQLSERKASQSVVDLVAKGIPKAGKISARGNGESNPVT 305					
Db	252 LDPKDGSAVVLGTYTRIGSDAYNQLSERKASQSVVDLYLISKGPSPDKISARGNGESNPVT 311					
RESULT 13	OMPA_SALTY STANDARD; PRT; 350 AA.					
ID	OMPA_SALTY ID P02936;					
AC	AC P02936; Last sequence update) (Outer membrane protein 33K) (Outer membrane major heat-modifiable protein).					
DT	DT 21-JUL-1986 (Rel. 01, Created)					
DT	DT 28-FEB-2003 (Rel. 41, Last sequence update)					
DT	DT 13-SEP-2005 (Rel. 48, Last annotation update)					
DE	Outer membrane protein A precursor (Outer membrane major heat-modifiable protein).					
GN	Name=ompA; OrderedLocusNames=STM1070;					
OS	Salmonella typhimurium.					
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.					
OX	NCBI_TaxID=602; OX NCBI_TaxID=602;					
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].					
RX	RX MEDLINE=83287368; PubMed=6349993;					
RA	RA Freudl, R., Cole, S.T.;					
RT	RT "Cloning and molecular characterization of the outer membrane protein A precursor (Outer membrane major heat-modifiable protein)."					
RN	RN [1] _					
RN	RN Nucleotide sequence [large scale genomic DNA].					
RX	RX MEDLINE=2154948; PubMed=11677609; DOI=10.1038/35101614;					
RA	RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latrelle P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,					

RA	Waterson R., Wilson R.K.; "Complete genome sequence of <i>Salmonella enterica</i> serovar Typhimurium LT2," <i>Nature</i> 413:852-856(2001).	Qy	126 STGVSSEHDTEGVSPVAGGYEWAVTRDIATRLEYWVNNGCAGTGTGTRPDNGMLSLGV 185
RT	- ; FUNCTION: Required for the action of colicins K and L and for the stabilization of mating aggregates in conjugation. Serves as a receptor for a number of T-even like phages. Also acts as a porin with low permeability that allows slow penetration of small solutes (BY similarity).	Db	133 G-GPSTKHDIGTGSVPAGGYAIPBIAITLKQDLYTOLSN 191
CC	- ; SUBUNIT: Monomer (Probable).	Qy	186 SYRFQQDAAPVVAAPAPAPAEVATKHTFLKSVDLFNFNKATLKPECGOALDOLYTLNSN 245
CC	- ; SIMILARITY: Belongs to the OmpA family.	Db	192 SYRFQQDAAPVVAAPAPAPEVQTFLKSVDLFNFNKSTLKPBCQALDOLYSOLSN 251
CC	- ; SIMILARITY: Contains 1 OmpA-like domain.		
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.		
CC	EMBL: XCA006; CAAI6037.1; - ; Genomic DNA.		
DR	EMBL; AB008746; AL20003.1; - ; Genomic_DNA.		
DR	PIR; A01436; MMDBAT.		
DR	HSSP; P02934; 1Q0P.		
DR	SMR; P0936; 2E-201.		
DR	StryGene; SG10263; OmpA.		
DR	InterPro; IPR00664; Bac_OmpA.		
DR	InterPro; IPR002358; OmpA.		
DR	InterPro; IPR00665; OMPA/MotB.		
DR	InterPro; IPR00666; OMPA_LIKE.		
DR	InterPro; IPR000438; OmpA_trem.		
DR	Pfam; PF00691; OmpA.		
DR	PRINTS; PRO1021; OMPADOMAIN.		
DR	PRINTS; PR01022; OUTMRMBRANA.		
DR	PRODOM; PD000930; OmpA/MotB_1.		
DR	PROSITE; PS01068; OMPA_1; 1.		
DR	PROSITE; PS51123; OMPA_2; 1.		
KW	Complete Proteome; Conjugation; Ion transport; Membrane; Outer membrane; Phage recognition; Porin; Repeat; Signal; Transmembrane; Transport.		
SIGNAL	1		
FT	CHAIN 22 350		
FT	TRANSMEM 27 40		
FT	TRANSMEM 55 67		
FT	TRANSMEM 70 85		
FT	TRANSMEM 97 107		
FT	TRANSMEM 111 126		
FT	TRANSMEM 146 157		
FT	TRANSMEM 163 179		
FT	TRANSMEM 185 196		
FT	REPEAT 205 206		
FT	REPEAT 207 208		
FT	REPEAT 209 210		
FT	REPEAT 211 212		
FT	DOMAIN 214 234		
FT	REGION 205 212		
FT	DISULFID 315 327		
FT	CONFFLICT 1.14 1.14		
FT	SEQUENCE 350 AA; 37515 MW;		
FT	B4AC52C8C5DF54FE CRC64;		
FT	Score 1495; DB 1; Length 350;		
FT	Pred. No. 2e-106; Indels 6; Gaps 2;		
FT	Best Local Similarity 82.8%; Conservative 26%; Mismatches 26;		
FT	Query Match 82.0%; Score 1495; Pred. No. 2e-106; Indels 6; Gaps 2;		
FT	Best Local Similarity 83.7%; Pred. No. 9.4e-106; Mismatches 282; Conservative 17;		
FT	Matches 282; Conservatve 17; Mismatches 32; Index 6; Gaps 2;		
FT	6 VLNAPKONTWYAGGKLGSQHDTGFGNGFQNNGPTRNLDOLGAGAFGGYQVNPNVLF 65	Oy	6 VLNAPKONTWYAGGKLGSQHDTGFGNGFQNNGPTRNLDOLGAGAFGGYQVNPNVLF 65
FT	18 VAQAPKONTWYAGKLGNSQHDTGF1----HNDRMHENOLGAGAFGGYQVNPNVLF 72	Db	18 VAQAPKONTWYAGKLGNSQHDTGF1----HNDRMHENOLGAGAFGGYQVNPNVLF 72
FT	6 EMGYDWLGRMAYKGSVDNGAFAKGQVQLTAKLGYPITDDYDTRLGMMWRADSCKNYA 125	Qy	6 EMGYDWLGRMAYKGSVDNGAFAKGQVQLTAKLGYPITDDYDTRLGMMWRADSCKNYA 125
FT	73 EMGYDWLGRMAYKGSVDNGAFAKGQVQLTAKLGYPITDDYDTRLGMMWRADSCKNYA 132	Db	73 EMGYDWLGRMAYKGSVDNGAFAKGQVQLTAKLGYPITDDYDTRLGMMWRADSCKNYA 132

Db	102	EMGYDWLGRMPYKCDNNINGAYAKAGCQVOLTAKLGTPITDDIYTRLGGMWRADTKANVP	161		DR PRINTS; PRO1021; OMPADOMAIN.
Db	126	STGVRSERHDGTGSPVPGGEWAIVTDATRLLEYQWVNNGDAGTGTGTRPDNGMLSLGV	185		DR PRINTS; PRO1022; OUTREMBRANE.
Db	162	G-SASFQKDHTGTGSPVPGGEWAIVTDATRLLEYQWVNNGDAGTGTGTRPDNGMLSLGV	220	KW Complete proteome.	DR PRODTB; PS010568; OMPA; 1.
Db	221	SIRFGQGEVAPVVAAPAPAPEVOTKHTFLKSDFLFTFNKATLKEFQQAQLDQLYSQLSN	280	SEQUENCE 348 AA;	DR SEQUENCE 348 AA; 37283 MW; 42623.67041.D62F4 CRC64;
Qy	186	SYFGQEDAAPVVAAPAPAPEVATKHTFLKSDFLFTFNKATLKEFQQAQLDQLYTLSN	245	Query Match 80.8%; Score 1473; DB 2; Length 348;	DR Best Local Similarity 83.4%; Pred. No. 9.9e-105;
Qy	281	LDPKGDSVAVLGYTDIGRSAYNQOLSEKRAQSUVVDYLIVAKGIPAKTISARGMGESENPT	305	Matches 281; Conservative 18; Mismatches 50	DR Matches 281; Conservative 18; Mismatches 50
Qy	306	GNTCDNYKARAAALIDCLAPDRRYVEIEVKYKEVVTQ	342	Qy 6 VLNDAKDNTWYAGKLGWSOYHDTGFYNGFQNNNGPDRNDLACAGGCGYQVNPNLGF	DR Qy 6 VLNDAKDNTWYAGKLGWSOYHDTGFYNGFQNNNGPDRNDLACAGGCGYQVNPNLGF
Qy	341	GNTCDNYKQRAALIDCLAPDRRYVEIEVKYKEVVTQ	377	Qy 18 VQAQPKDNTWYTGAULGWSOYHDTGF1----PNNGTPHENOLGAGAGFGGYQVNPNYVG	DR Qy 18 VQAQPKDNTWYTGAULGWSOYHDTGF1----PNNGTPHENOLGAGAGFGGYQVNPNYVG
Db	281	LDPKGDSVAVLGYTDIGRSAYNQOLSEKRAQSUVVDYLIVAKGIPAKTISARGMGESENPT	340	Qy 66 EMGYDWLGRMAYKGSVONGAFKAQGVQLTAKLGYPITDDIYTRLGGMWRADSGNYA	DR Qy 66 EMGYDWLGRMAYKGSVONGAFKAQGVQLTAKLGYPITDDIYTRLGGMWRADSGNYA
Db	126	STGVSRSEBDTGSPVPGGEWAIVTDATRLLEYQWVNNGDAGTGTGTRPDNGMLSLGV	185	Qy 73 EMGYDWLGRMYPKGDNINGAYKAQGVQLTAKLGYPITDDIYTRLGGMWRADSGNYA	DR Qy 73 EMGYDWLGRMYPKGDNINGAYKAQGVQLTAKLGYPITDDIYTRLGGMWRADSGNYA
Db	133	G-GASFKDHDTCVSPVPGGEWAIVTDATRLLEYQWVNNGDANTIGTRPDNGMLSLGV	191	Qy 126 STGVSRSEBDTGSPVPGGEWAIVTDATRLLEYQWVNNGDAGTGTGTRPDNGMLSLGV	DR Qy 126 STGVSRSEBDTGSPVPGGEWAIVTDATRLLEYQWVNNGDAGTGTGTRPDNGMLSLGV
Db	186	SYRFQGDDAAPVAPAPAPAPAWATKFTLKSDFLTFNFKATLKEFQQAQLDQLYTLSN	245	Qy 133 G-GASFKDHDTCVSPVPGGEWAIVTDATRLLEYQWVNNGDANTIGTRPDNGMLSLGV	DR Qy 133 G-GASFKDHDTCVSPVPGGEWAIVTDATRLLEYQWVNNGDANTIGTRPDNGMLSLGV
Db	192	SYRFQGEEAAPV--AAPAPAEVOTKHTFLKSDFLTFNFKATLKEFQQAQLDQLYTLSN	249	Qy 186 SYRFQGDDAAPVAPAPAPAWATKFTLKSDFLTFNFKATLKEFQQAQLDQLYTLSN	DR Qy 186 SYRFQGDDAAPVAPAPAPAWATKFTLKSDFLTFNFKATLKEFQQAQLDQLYTLSN
Db	246	MDPKDGSAAVVLGTYDRIGSEAYNQOLSEKRAQSUVVDYLIVAKGIPAKTISARGMGBSNPVT	305	Qy 192 SYRFQGEEAAPV--AAPAPAEVOTKHTFLKSDFLTFNFKATLKEFQQAQLDQLYTLSN	DR Qy 192 SYRFQGEEAAPV--AAPAPAEVOTKHTFLKSDFLTFNFKATLKEFQQAQLDQLYTLSN
Db	250	LDPKGDSVAVLGYTDIGRSAYNQOLSEKRAQSUVVDYLIVAKGIPAKTISARGMGBSNPVT	342	Qy 246 MDPKDGSAAVVLGTYDRIGSEAYNQOLSEKRAQSUVVDYLIVAKGIPAKTISARGMGBSNPVT	DR Qy 246 MDPKDGSAAVVLGTYDRIGSEAYNQOLSEKRAQSUVVDYLIVAKGIPAKTISARGMGBSNPVT
Db	310	GNTCDNYKORAAALIDCLAPDRRYVEIEVKYKEVVTQ	346	Qy 250 LDPKGDSVAVLGYTDIGRSAYNQOLSEKRAQSUVVDYLIVAKGIPAKTISARGMGBSNPVT	DR Qy 250 LDPKGDSVAVLGYTDIGRSAYNQOLSEKRAQSUVVDYLIVAKGIPAKTISARGMGBSNPVT
Db	310	GNTCDNYKORAAALIDCLAPDRRYVEIEVKYKEVVTQ	346	Qy 306 GNTCDNYKARAAALIDCLAPDRRYVEIEVKYKEVVTQ	DR Qy 306 GNTCDNYKARAAALIDCLAPDRRYVEIEVKYKEVVTQ
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SEARCH		Job time : 232 secs			
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Q83RX2_SHIFL					
ID Q83RX2_1_Q7UD17;					
DT 01-JUN-2003 (TREMBLrel. 24, Created)					
DT 01-JUN-2003 (TREMBLrel. 31, Last sequence update)					
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)					
DE Outer membrane protein 3a (II; G,d)					
GN Name=ompA OrderedLocusNames=S1023, SF0957;					
OS Shigella flexneri					
OC Bacteria; Gammaproteobacteria; Enterobacteriales;					
OC Enterobacteriaceae; Shigellaceae;					
RN NCBI_TaxID=623;					
RN NCBI_TaxID=623;					
RP NUCLEOTIDE SEQUENCE.					
RC STRAIN=301 / Sequence 2a,					
RX MEDLINE=2222406; published=12384590; DOI=10.1093/nar/gkf566;					
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,					
RA Yang J., Yang F., Zhang J., Wu H., Qu D., Dong J.,					
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,					
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,					
RA Yu J.;					
RT "Genome sequence of <i>Shigella flexneri</i> 2a: insights into pathogenicity through comparison with genomes of <i>Escherichia coli</i> K12 and O157.";					
[2]					
RT NUCLEOTIDE SEQUENCE.					
RC STRAIN=24577 / ATCC 700930 / Serotype 2a;					
RX MEDLINE=22530274; Published=12704152;					
RX DOI=10.1128/JAI.71.5.2775-2786.2003;					
RA Wei J., Goldberg M.B., Burdick V., Venkatesan M.M., Deng W.,					
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,					
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,					
RA Schwartz D.C., Blattner F.R.,					
RA "Complete genome sequence and comparative genomics of <i>Shigella flexneri</i> serotype 2a strain 24577."					
RT Infec. Immun. 71:2775-2786 (2003).					
RL EMBL; AE056574; AAN42386.2; -; Genomic_DNA.					
DR EMBL; AE016981; AAP16471.1; -; Genomic_DNA.					
DR HSSP; P02934; 18XW.					
DR SMR; Q83RX2; 22-201.					
DR GO; GO:0016021; C:integral to membrane; IEA.					
DR GO; GO:002379; C:outer membrane (sensu Gram-negative Bacteria); IEA.					
DR GO; GO:0005198; F:structural molecule activity; IEA.					
DR InterPro; IPR006664; Bac_OmpA.					
DR InterPro; IPR001035; MotY.					
DR InterPro; IPR002368; OmpA.					
DR InterPro; IPR006665; OmpA/MotB.					
DR InterPro; IPR006690; OmpA_LIKE.					
DR InterPro; IPR000498; OmpA_tmem.					
DR Pfam; PF00919; OmpA; 1.					
DR Pfam; PF01380; OmpA_memebrane.					
DR Prints; PRO1023; NAFLumbrane; 1.					

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Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6
OM protein - protein search, using sw model	
Run on:	November 25, 2005, 23:59:49 ; Search time 40 Seconds 827.464 Million cell updates/sec
Title:	US-09-013-772A-2
Perfect score:	1823
Sequence:	1 MKAIFVLNAAPKDNTWYAGG..... DRRVEIEVKGYKEVVTQPAQ 344
Scoring table:	BLOSUM62
Gapcost:	10.0 , Gapext 0.5
Searched:	283416 seqs, 96226763 residues
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## ALIGNMENTS

## RESULT 1

JC6558

outer membrane protein A precursor - Klebsiella pneumoniae

C.Species: Klebsiella pneumoniae

C.Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 07-May-1999

C.Accession: JC6558

R.Nguyen, T.N.; Samuelson, P.; Sterky, F.; Merle-Poitte, C.; Robert, A.; Bausant, T.; H

Gene 210, 93-101, 1998

A.Title: Chromosomal sequencing using a PCR-based biotin-capture method allowed isolation

A.Reference number: JG6558; MUID:98192544; PMID:9524233

A.Accession: JC6558

A.Molecule type: DNA

A.Residues: 1-356 &lt;NGU&gt;

A.Cross-references: UNIPARC:UPI00001780DF

A.Experimental source: IP I145

C.Genetics:

C.Superfamily: outer membrane protein A

C.Keywords: membrane protein

F1-21/Domain: signal sequence #status predicted &lt;SIG&gt;

F22-356/Product: outer membrane protein A #status predicted &lt;MAT&gt;

Result No.	Score	Query Match	Length	DB ID	Description
1	1702	97.8	356	JC6558	outer membrane pro
2	15612	84.6	350	S07222	outer membrane pro
3	15255	83.7	351	MMEBAD	outer membrane pro
4	15151	82.7	346	1 MMEBCA	outer membrane pro
5	15111	82.9	346	2 A90759	outer membrane pro
6	15111	82.9	346	2 G85622	outer membrane pro
7	1439	82.2	350	2 A10626	outer membrane pro
8	1400	81.7	350	1 MMEBAT	outer membrane pro
9	1381	75.8	359	2 S07228	outer membrane pro
10	1325.5	72.7	353	2 AD0175	probable outer mem
11	1128	61.9	238	2 I62385	outer membrane pro
12	1112.5	61.0	244	2 I62383	outer membrane pro
13	1111	60.9	243	2 I62388	outer membrane pro
14	1100.5	60.9	244	2 I62389	outer membrane pro
15	1109	60.8	243	2 I8451	outer membrane pro
16	1106	60.7	243	2 I62386	outer membrane pro
17	1089	59.7	241	2 I62287	outer membrane pro
18	1084	59.5	241	2 I62391	outer membrane pro
19	1074.5	58.9	240	2 I62394	outer membrane pro
20	1056.5	58.0	238	2 I40703	outer membrane pro
21	646.5	35.5	353	2 C64187	outer membrane pro
22	51.5	28.3	349	2 B84968	outer membrane pro
23	443.5	24.3	321	2 F82104	outer membrane pro
24	271	14.9	194	2 A45275	21K outer membrane pro
25	262	14.4	236	2 A27894	outer membrane pro
26	255	14.0	242	2 C81205	outer membrane pro
27	251	13.8	240	2 A37004	outer membrane clu
28	250	13.7	242	2 A81792	outer membrane pro
29	243	13.3	326	2 S04934	root adhesin - pse

## RESULT 2

F;201-213/Region: alanine/proline-rich  
 F;214-351/Domain: periplasmic #status predicted <PER>

Query Match	83.7%	Score 1525.5	DB 1	Length 351;
Best Local Similarity	84.6%	Pred. No. 3.2e-108;		
Matches 285; Conservative		Mismatches 27;	Indels 5;	Gaps 1;

Qy 6 VLNAAPKDNTWYAGKLGSQYHDTGPFVNGFQNNGPTRNDLGAFAFGGYQVNPFYLG 65  
 Db 18 VQAAPKDNTWYAGKLGSQYHDTGPFVNGFQNNGPTRNDLGAFAFGGYQVNPFYLG 72

Qy 66 ENGYDWLGRMAYKGSVDNGFAKAQGVOLTAKLKGYPITDDLYTRLCMVYRADSKGNYA 125  
 Db 73 ENGYDWLGRMYPKGSVENGAYAQGVOLTAKLKGYPITDDLYTRLCMVYRADSKHNN 132

Qy 126 SYRGQDAAPVAPAPAPAVKHTFLKSVDLFENFKATLKPEGQALDOLYTQLSN 245  
 Db 133 VTGESEKQHDTGSPVFAGGWEAWTPEIATLKQYQWTNNIGDAHTIGTRDNLGLSIGV 192

Qy 186 SYRFQGDAAPVAPAPAPAVKHTFLKSVDLFENFKATLKPEGQALDOLYTQLSN 245  
 Db 193 SYRFQGDAAPVAPAPAPAVKHTFLKSVDLFENFKATLKPEGQALDOLYSQLSN 252

Qy 246 MDPKDGSAVVLGYTDIGSEAYNQLSKSEKRAQSVDVYLVAKGIPAGKISARGMGESENPT 305  
 Db 253 LDPKDGSVVLGYTDIGSDAYNQLSERRAQSVVDYLISKTPADKISARGMGESENPT 312

Qy 306 GNTCDNVVKARALIDCLAPDRVEIEVKGKEVVTQP 342  
 Db 313 GNTCDNVVKQRALIDCLAPDRVEIEVKGKEVVTQP 349

RESULT 4

Db 77 EMGDWLGRMAYKGSVDNGFAKAQGVOLTAKLKGYPITDDLYTRLCMVYRADSKYNA 125  
 Db 77 EMGDWLGRMAYKGSVDNGFAKAQGVOLTAKLKGYPITDDLYTRLCMVYRADSKYNA 125  
 Db 126 STGVSRSSEHDTGSPVFAGGWEAVTRDIAATRLEYQWTNNIGDAGTYGTRDNGMLSIGV 185  
 Db 132 SNSIAGDNHDHTGSPVFAGGWEAVTRDIAATRLEYQWTNNIGDAGTYGTRDNGMLSIGV 191

Qy 186 SYRGQDAAPVAPAPAPAVKHTFLKSVDLFENFKATLKPEGQALDOLYTQLSN 245  
 Db 192 SYRGQEDAAPVAPAPAPAVKHTFLKSVDLFENFKATLKPEGQALDOLYTQLSN 251

Qy 246 MDPKDGSAVVLGYTDIGSEAYNQLSKSEKRAQSVDVYLVAKGIPAGKISARGMGESENPT 305  
 Db 252 MDPKDGSAVVLGYTDIGSEQYQNLSEKRAQSVDVYLVAKGIPAGKISARGMGESENPT 311

Qy 306 GNTCDNVVKARALIDCLAPDRVEIEVKGKEVVTQP 342  
 Db 312 GNTCDNVVKARALIDCLAPDRVEIEVKGKEVVTQP 348

RESULT 3

MNEBAD  
 outer membrane protein A precursor - *Shigella dysenteriae*  
 C;Species: *Shigella dysenteriae*  
 C;Date: 18-Aug-1982 #sequence\_revision 18-Aug-1982 #text\_change 09-Jul-2004  
 C;Accession: A03435  
 R;Braun, G.; Cole, S.T.  
 Nucleic Acids Res. 10, 2367-2378, 1982.  
 A;Title: The nucleotide sequence coding for major outer membrane protein OmpA of *Shigella dysenteriae*.  
 A;Reference number: A03435; MUID: 82221414; PMID: 6283478

A;Accession: A03435  
 A;Molecule type: DNA  
 A;Cross-references: UNIPARC:UPI0000130CFA;  
 A;Experimental source: K12, strain K80  
 R;Chen, R.; Schmidmayer, W.; Kramer, C.; Chen-Schmidmayer, U.; Henning, U.  
 Proc. Natl. Acad. Sci. U.S.A. 77, 4592-4596, 1980  
 R;Kuhn, A.; Kiefer, D.; Kohne, C.; Zhu, H.Y.; Tschantz, W.R.; Dalbey, R.E.  
 Eur. J. Biochem. 226, 891-897, 1994  
 A;Title: Evidence for a loop-like insertion mechanism of pro-Omp A into the inner membran  
 A;Reference number: S50909; MUID: 95112855; PMID: 7813480

C;Keywords: transmembrane protein  
 C;Superfamily: outer membrane protein A  
 C;Genetics:  
 C;Cross-references: UNIPROT:P02935; UNIPARC:UPI0000130CFA;  
 C;Species: outer membrane protein A  
 C;Keywords: outer membrane protein A #status predicted <SIG>  
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 F;22-201/Domain: intramembrane #status predicted <INT>

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A;Cross-references: UNIPARC:UPI00001747C	
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cole, R.A.; Rose, D.J.; Maurer, B.; Shao, Y.	
Science 277, 1453-1462, 1997	
A;Title: The complete genome sequence of Escherichia coli K-12.	
A;Reference number: A64720; MUID:97426617; PMID:9278503	
A;Status: nucleic acid sequence not shown; translation not shown	
A;Experimental source: strain K-12, substrate MG1655	
A;Gene: ompA; tolG; tut; con	
A;Map position: 22 min	
A;Residues: 1-346 <BLAT>	
A;Cross-references: UNIPARC:UPI0000130CF0; GB:AE000198; GB:U00096; NID:91787189; PIDN:AA	
A;Accession: D6436	
A;Status: nucleic acid sequence not shown; translation not shown	
A;Molecule type: DNA	
A;Genes: ompA; tolG; tut; con	
A;Map position: 22 min	
[REDACTED] description: required for the action of colicins K and L and for the stabilization of diffusion channels that allow penetration of various solutes	
C;Keywords: outer membrane protein A	
C;Keywords: membrane protein; monomer	
P;1-21/Domain: signal sequence #status predicted <SIG>	
P;22-346/Domain: outer membrane protein A #status predicted <MAT>	
P;22-196/Domain: intramembrane #status predicted <NT>	
P;196-208/Region: alanine/proline-rich	
P;209-346/Domain: periplasmic #status predicted <PER>	
P;257-301/Domain: ompA-like domain #status predicted <OMP>	
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Best Local Similarity 84.9%; Pred: No 3.9@10;	
Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;	
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Db 18 VAQAAPKDNTWYTGAKGQWSOYHDITGFI----NNNGTHENLQAGAAGGGQVNPIVYGF 72	
Qy 66 EMGYDWLGRCMAYKGSVNDGFAKAQGVQLTAKGYPITDDLYTRLGCMWVRADSKGNYA 1.25	
Db 73 EMGYDWLGRCMYPKGSVENGAY&QGVQLTAKGYPITDDLYTRLGCMWVRADTSKN-- 130	
Qy 126 STGVSRSEHDGTGVSPVFGGVEWAVTRDIATRLEYQWNNGPQAGTYGTRPDNGMLSLGV 185	
Db 131 --VYGKHDIGVSPVFGGVEAIPPEIATRLEYQWNNGPQAGTYGTRPDNGMLSLGV 1.87	
Qy 186 SYRFQGEDAAPVYAPAPAPAPAPAPAPYQKHTFLKSDVLENFKNATLKPEQOALDOLYTQLSN 245	
Db 188 SYRFQGEDAAPVYAPAPAPAPAPYQTKHETFLKSDVLENFKNATLKPEQGAALDOLYQSQLSN 247	
Qy 246 MDPKDGSAVLVGLYTDRIGSEANQQLSERKASQVVDYLVAKGIPAKTSARGMGESENVPVT 3.05	
Db 248 LDPKDGSUVVVLVGLYTDRIGSDAVNOGLSERRAQSVVDYLISKGIPAKTSARGMGESENVPVT 307	
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Db 308 GNTCDNIVKORAALIDCLAPDRRVEIEVKYKEYVVTQP 344	
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A90759 Outer membrane protein 3a ECs1041 [imported] - Escherichia coli (strain O157:H7, substra	
C;Species: Escherichia coli	
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004	
C;Accession: A90759	
R;Hayashi, T.; Makino, K.; Ueda, T.; Kohara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.	
Gasawara, N.; Yasunaga, T.; Kohara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.	
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene	
A;Reference number: A99629; MUID:21156231; PMID:11258796	
A;Accession: A90759	
A;Status: preliminary	
A;Molecule type: DNA	
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Qy	246	MDPDKGSVAVLGTYDRIGSEAYNQOLSERAQSVVDLYAKGIPAGKTSARGMGESENPT	305	A; Accession: A03436
	:      :      :      :      :      :    :    :    :    :    :		A; Molecule type: DNA	
	A; Residues: 1-350 <PBR>		C; Cross-references: UNIPROT: P02936; UNIPARC: UP100001703A0; GB: X02006; NID: 947798; PIDN: CI	
Db	248	LDPDKGSVVLGYDRIGSDAYNGLSERAQSVVDLYAKGIPAGKTSARGMGESENPT	307	C; Genetics:
Qy	306	GNTCDNVKVARAALIDCLADPDRVIEVKYKEVVTQP	342	A; Gene: ompA
Db	308	GNTCDNVKVARAALIDCLADPDRVIEVKYKEVVTQP	344	A; Map position: 20 min
			C; Function:	
			A; Description: required for the action of colicins and for the stabilization of mat. i.e.	
			A; Note: cannot serve as the receptor for the ompA-specific phage K3 and T4II	
			C; Keywords: transmembrane protein	
			C; Superfamily: outer membrane protein A	
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Db	18	VAQAAPKDNTWYAGKLGWSQYHDTGYNGFQNNNGPTRNDLGAGAFGGYQVNPNYLGF	72	Db 18 VAQAAPKDNTWYAGKLGWSQYHDTGYNGFQNNNGPTRNDLGAGAFGGYQVNPNYLGF 72
			66 ENGYDWLGMRAYGSVNGAFAKGQVLTAKGYPFDLDIYTRGGMWNRADSKGNYA 125	
			73 EMGYDWLGMRPYKGDNINGAYKAQGQVLTAKGYPFDLDIYTRGGMWNRADSKGNYA 132	
Qy	126	STGVSRSEHDHTGVSPVFGGWEAVTRDIAATRLEYQVNNGIDAGTVTRPDNGMLSLGV	185	Qy 126 STGVSRSEHDHTGVSPVFGGWEAVTRDIAATRLEYQVNNGIDAGTVTRPDNGMLSLGV 185
Db	133	G-GPSTKDHDTCVSPVFGGWEAVTRDIAATRLEYQVNNGIDAGTVTRPDNGMLSLGV	191	Db 133 G-GPSTKDHDTCVSPVFGGWEAVTRDIAATRLEYQVNNGIDAGTVTRPDNGMLSLGV 191
			186 SYRFGQEDAAPVVAAPAPAPAEVATKHFPLKSDVLFNPKATLKPEEQQALDQLYTQLSN 245	
			192 SYRFGQEDAAPVVAAPAPAPAEVATKHFPLKSDVLFNPKATLKPEEQQALDQLYTQLSN 251	
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Qy	66	EMGYDWLGMRAYGSVNGAFAKGQVLTAKGYPFDLDIYTRGGMWNRADSKGNYA 125		Qy 66 EMGYDWLGMRAYGSVNGAFAKGQVLTAKGYPFDLDIYTRGGMWNRADSKGNYA 125
Db	73	EMGYDWLGMRPYKGDNINGAYKAQGQVLTAKGYPFDLDIYTRGGMWNRADSKGNYA 132		Db 73 EMGYDWLGMRPYKGDNINGAYKAQGQVLTAKGYPFDLDIYTRGGMWNRADSKGNYA 132
Qy	126	STGVSRSEHDHTGVSPVFGGWEAVTRDIAATRLEYQVNNGIDAGTVTRPDNGMLSLGV	185	Qy 126 STGVSRSEHDHTGVSPVFGGWEAVTRDIAATRLEYQVNNGIDAGTVTRPDNGMLSLGV 185
Db	133	G-GASTKDHDTCVSPVFGGWEAVTRDIAATRLEYQVNNGIDAGTVTRPDNGMLSLGV	191	Db 133 G-GASTKDHDTCVSPVFGGWEAVTRDIAATRLEYQVNNGIDAGTVTRPDNGMLSLGV 191
			186 SYRFGQEDAAPVVAAPAPAPAEVATKHFPLKSDVLFNPKATLKPEEQQALDQLYTQLSN 245	
			192 SYRFGQEDAAPVVAAPAPAPAEVATKHFPLKSDVLFNPKATLKPEEQQALDQLYTQLSN 251	
Qy	246	MDPDKGSVAVLGTYDRIGSEAYNQOLSERAQSVVDLYAKGIPAGKTSARGMGESENPT	305	Qy 246 MDPDKGSVAVLGTYDRIGSEAYNQOLSERAQSVVDLYAKGIPAGKTSARGMGESENPT 305
Db	252	LDPDKGSVVLGYDRIGSDAYNGLSERAQSVVDLYAKGIPAGKTSARGMGESENPT	311	Db 252 LDPDKGSVVLGYDRIGSDAYNGLSERAQSVVDLYAKGIPAGKTSARGMGESENPT 311
Qy	306	GNTCDNVKVARAALIDCLADPDRVIEVKYKEVVTQP	342	Qy 306 GNTCDNVKVARAALIDCLADPDRVIEVKYKEVVTQP 342
Db	312	GNTCDNVKVARAALIDCLADPDRVIEVKYKEVVTQP	348	Db 312 GNTCDNVKVARAALIDCLADPDRVIEVKYKEVVTQP 348

RESULT 8

MMBET

outer membrane protein A precursor - *Salmonella typhimurium*

N

Alternative names: outer membrane major heat-modifiable protein; outer membrane protein

C; Species: *Salmonella typhimurium*

C; Date: 19-Feb-1984 #sequence\_revision 19-Feb-1984 #text\_change 09-Jul-2004

C; Accession: A03436

C; Title: Cloning and molecular characterization of the *ompA* gene from *Salmonella typhimurium*

C; Author: R. Preudi, R. Cole, S.T. Cole, 1983

C; Abstract: Cloning and molecular characterization of the *ompA* gene from *Salmonella typhimurium*

MMBET

outer membrane protein A

C

Keywords: membrane protein

F1-21/Domain: signal sequence #status predicted &lt;SIG&gt;

F1-22-230/Domain: outer membrane protein ompA #status Predicted &lt;MAT&gt;

F1-22-230/Domain: intramembrane #status predicted &lt;INT&gt;

F1-210-219/Region: alanine/proline-rich

F1-220-359/Region: periplasmic #status predicted &lt;PER&gt;

C; Genetics:

A; Gene: ompA

A; Molecule type: DNA

A; Residues: 1-359 &lt;BR&gt;

A; Cross-references: UNIPROT: P04845; UNIPARC: UP10000130CF8; EMBL: X0061B; NID: 947742; PIDN

Query Match Score 75.8%; Length 1381.5; DB 2; Length 359;

Best Local Similarity	78.2%	Pred. No.	2.7e-97;
Matches	269;	Mismatches	44;
Qy	6	VLNAAPKDNTWYAGGKLGNMSEOHDTGPFYNGFQN - NNGPTNDOLGAGFGGYQVNPYL	63
Db	18	VAQAAPKDNTWYAGGKLGNMSEOHDTGPFYNGFQN - NNGPTNDOLGAGFLGQANQYL	77
Qy	64	GFBNGDYWLGRMA YKGSVDNAGFAKGQVQTLAKGQVTPITDDIYTRLGGMWWRADSKN	123
Db	78	GFEGLGYWLGRMPYKGSVNNGFAKGQVQLAALKSYPADDLIDYTRLGGMWWRADSKN	137
Qy	124	YASTGVSRSEHDITGSPVPAAGVWEAVTRDIATRLEYOYNINIGDAGTICTRPNDGMLSL	183
Db	138	YGRGQRLSDHDTGCVSPLAAGVETALTRKWAATRDYQFSNIGDAGTICARPDTMILSL	197
Qy	184	GVSYRFQGD - AAVPVAPAPAPAPEVATKFTLSDVLENFKENATLKPEQSQALDQLYQ	242
Qy	198	GVSYRFQGDQDVVAP - AAVPVAPAPVETKFTLSDVLENFKENSTLKAESQQALDQLYQ	255
Qy	243	LSNNPDKGDSAVVLYDRIGSEAYNOOLSERKASQSVNDYLVAKGIPAGKISARGMGESEN	302
Db	256	LSNNPDKGSSVVVLYGTDAGSDQYNQKLSERQASQVVDLVLVKGIPSXKISARGMGEAD	315
Qy	303	PVTGNTCDVNWKARA - ALIDCLAPDRRVTEVKGYKEYNTQPG	344
Db	316	AVTGNTCGYKSGRATKAQIVCLAPDRRVTEVKGITKDVTQPG	359
RESULT 10			
AD0175		probable outer membrane porin A protein ompA [imported] - Yersinia pestis (strain C992)	
C: Species	Yersinia pestis		
C: Date	02-Nov-2001	#text_change 09-Jul-2004	
C: Accession	AD0175		
R: Parikhil, J.; Wren, B. W.; Thomson, N. R.; Tritball, R. W.; Holden, M. T. G.; Prentice, M. B.; deno-Terrall, A. M.; Chillingworth, T.; Cronin, A.; Davies, R. M.; Davis, P.; Dougan, G.; ill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; Nature 413, 523-527, 2001			
A: Title	Genome sequence of Yersinia pestis, the causative agent of plague.		
A: Reference number	AB0001; PMID:21470413; PMID:11586360		
A: Status	preliminary		
A: Molecule type	DNA		
A: Residues	1-353 <KUR>		
A: Cross-references	UNIPROT:Q8ZG77; UNIPARC:UPI00000CD7EA; GB:AL590842; PIDN: CAC90263.1; EBI: Q92332		
C: Gene	ompA		
C: Superfamily	outer membrane protein A		
Query Match	72.7%	Score	1325.5; DB 2; Length 353;
Best Local Similarity	75.2%	Pred.	No. 4.8e-93; Mismatches 28; Indels 49; Gaps 4;
Qy	6	VLNAAPKDNTWYAGGKLGNMSEOHDTGPFYNGFQNNGPTNDOLGAGFGGYQVNPYL	65
Db	18	VAQAAPKDNTWYAGGKLGNMSEOHDTGPFYNGFQNNGPTNDOLGAGFLGQANQYL	73
Qy	66	EMGYDWLRMAYKGSVDNGFAKGQVQTLAKGQVTPITDDIYTRLGGMWWRADSKN	125
Db	74	EMGYDWLRMAYKGVDINGANGFAKGQVQTLAKGQVTPITDDIYTRLGGMWWRADSKN	132
Qy	126	STGYSR - SEHDITGSPVPAAGVWEAVTRDIATRLEYOYNINIGDAGTICTRPNDGMLSLG	184
Db	133	DGGGLDRASGHDTGSPVLAAGVETALTRKWAATRDYQFSNIGDAGTICARPDTMILSLV	192
Qy	185	VSYRFQGD - AAVPVAPAPAPAPEVATKFTLSDVLENFKENATLKPEQSQALDQLYQ	243
Db	193	VSYRFQGDAAAPVAPAPVETKFTLSDVLENFKENSTLKAESQQALDQLYQ	252
Qy	244	SMDPKDGSASAVVLYDRIGSEAYNOOLSERKASQSVNDYLVAKGIPAGKISARGMGESN	303
Db	253	SSDPDKDGSASAVVLYDRIGSEAYNOOLSERKASQSVNDYLVAKGIPAGKISARGMGESN	312

C;Keywords: membrane protein  
F:104-115/Region: alanine/proline-rich

Query Match 61.0%; Score 1112.5; DB 2; Length 244;  
Best Local Similarity 87.2%; Pred. No. 4..2e-17;  
Matches 212; Conservative 15; Mismatches 1; Indels 1; Gaps 1;

Qy 93 LTAKLGYPTDDIYTRIGGMWRADESKGNVASTGVSRSEHTGVSPEFAGGVENAVTR 152  
Db 1 LTAKLGYPTDDIYTRIGGMWRADESKGNVASTGVSRSEHTGVSPEFAGGVENAVTR 152

Qy 153 DIATRLEYQWNNGIDAGTVGRTRPDNGMISLGYSYRFQ-QEDAAPVYAPAPAPEVATK 211  
Db 61 DIATRLEYQWNNGIDAGTVGRTRPDNGMISLGYSYRFQ-QEDAAPVYAPAPAPEVATK 210

Qy 212 HFTLKSDFVNFKATLKPEQQALDQLYTLQSNMPKDGSAVLVGYDRISSEAYNQQL 271  
Db 121 HFTLKSDFVNFKATLKPEQQALDQLYTLQSNMPKDGSAVLVGYDRISSEAYNQQL 180

Qy 272 SEKRAQSVDYLVAKGIPAKGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRVEIE 331  
Db 181 SEKRAQSVDYLVAKGIPAKGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRVEIE 240

332 VKG 334  
Db 241 VKG 243

RESULT 14  
I62389 outer membrane protein A - Escherichia vulneris (ATCC 33821) (fragment)

Db 162389 outer membrane protein A - Escherichia vulneris (ATCC 33821)  
N:Alternate names: outer membrane protein II  
C:Species: Escherichia vulneris  
A:Variety: ATCC 33821  
C:Date: 04-Sep-1997 #sequence\_revision 07-Nov-1997 #text\_change 09-Jul-2004  
C:Accession: I62389  
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.  
J:Gen. Microbiol. 137, 1911-1921, 1991  
A:Title: Molecular and evolutionary relationships among enteric bacteria.  
A:Reference number: I40701; MUID:92065255; PMID:1955870  
A:Accession: I62389  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-244 <RES>  
A:Cross-references: UNIPROT:Q99115; UNIPARC:UPI00000BBFLD; GB: M63349; NID:9146992; PIDN:/  
A:Experimental source: ATCC 33821  
C:Genetics:

A:Gene: ompA  
C:Superfamily: outer membrane protein A  
C:Keywords: membrane protein  
F:104-115/Region: alanine/proline-rich

Query Match 60.9%; Score 1110.5; DB 2; Length 244;  
Best Local Similarity 86.8%; Pred. No. 6e-77; Mismatches 15; Indels 1; Gaps 1;

Qy 93 LTAKLGYPTDDIYTRIGGMWRADESKGNVASTGVSRSEHTGVSPEFAGGVENAVTR 152  
Db 1 LTAKLGYPTDDIYTRIGGMWRADESKGNVASTGVSRSEHTGVSPEFAGGVENAVTR 60

Qy 153 DIATRLEYQWNNGIDAGTVGRTRPDNGMISLGYSYRFQ-QEDAAPVYAPAPAPEVATK 211  
Db 61 DIATRLEYQWNNGIDAGTVGRTRPDNGMISLGYSYRFQ-QEDAAPVYAPAPAPEVATK 210

Qy 212 HFTLKSDFVNFKATLKPEQQALDQLYTLQSNMPKDGSAVLVGYDRISSEAYNQQL 271  
Db 121 HFTLKSDFVNFKATLKPEQQALDQLYTLQSNMPKDGSAVLVGYDRISSEAYNQQL 180

Qy 272 SEKRAQSVDYLVAKGIPAKGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRVEIE 331  
Db 181 SEKRAQSVDYLVAKGIPAKGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRVEIE 240

332 VKG 334  
Db 241 VKG 243

RESULT 15  
I84531 outer membrane protein A - Escherichia fergusonii (ATCC 35469) (fragment)

Db 162389 outer membrane protein A - Escherichia fergusonii (ATCC 35469)  
N:Alternate names: outer membrane protein II  
C:Species: Escherichia fergusonii  
A:Variety: ATCC 35469  
C:Accession: I84531  
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.  
J:Gen. Microbiol. 137, 1911-1921, 1991  
A:Title: Molecular and evolutionary relationships among enteric bacteria.  
A:Reference number: I40701; MUID:92065255; PMID:1955870  
A:Accession: I84531  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-243 <RES>  
A:Cross-references: UNIPROT:P24747; UNIPARC:UPI0000130CF3; GB: M63352; NID:9146990; PIDN:/  
A:Experimental source: ATCC 35471  
A:Accession: I62392  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-243 <RES>  
A:Cross-references: UNIPARC:UPI0000130CF3; GB: M63353; NID:9146998; PIDN:AAA24240..1; PIDN:/  
A:Experimental source: ATCC 35472  
C:Genetics:  
C:Gene: ompA  
C:Superfamily: outer membrane protein A  
C:Keywords: membrane protein  
F:103-114/Region: alanine/proline-rich

Query Match 60.9%; Score 1111; DB 2; Length 243;  
Best Local Similarity 87.2%; Pred. No. 5..5e-77; Mismatches 18; Indels 0; Gaps 0;

Qy 93 LTAKLGYPTDDIYTRIGGMWRADESKGNVASTGVSRSEHTGVSPEFAGGVENAVTR 152  
Db 1 LTAKLGYPTDDIYTRIGGMWRADESKGNVASTGVSRSEHTGVSPEFAGGVENAVTR 60

Qy 153 DIATRLEYQWNNGIDAGTVGRTRPDNGMISLGYSYRFQ-QEDAAPVYAPAPAPEVATK 212  
Db 61 DIATRLEYQWNNGIDAGTVGRTRPDNGMISLGYSYRFQ-QEDAAPVYAPAPAPEVATK 210

Qy 213 FTLKSDFVNFKATLKPEQQALDQLYTLQSNMPKDGSAVLVGYDRIGSPEAYNQQL 272  
Db 121 FTLKSDFVNFKATLKPEQQALDQLYTLQSNMPKDGSAVLVGYDRIGSPEAYNQQL 180

A: Molecule type: DNA  
A: Residues: 1-243 <RES>  
A: Cross-references: UNIPROT:P24747; UNIPARC:UPI000016F6FB; GB:M63351; NID:9146982; PIDN:  
A: Experimental source: ATCC 35469  
C: Genetics:  
A: Gene: ompA  
C: Superfamily: outer membrane protein A  
C: Keywords: membrane protein  
F: 1.03-114/Region: alanine/proline-rich

Query Match 60.8%; Score 1109; DB 2; Length 243;  
Best Local Similarity 87.2%; Pred. No. 7\_7e-77;  
Matches 211; Conservative 13; Mismatches 18; Indels 0; Gaps 0;  
Qy 93 LTAKLGYPTDDDIYTRIGGMWRADESKGNYASTGVSRSEHDTGVSPVFAAGGVEAWTR 152  
Db 1 LTAKLGYPTDDDIYTRIGGMWRADESKGNYASTGVSRSEHDTGVSPVFAAGGVEAWTR 60  
Qy 153 DIATRLEYCWNNTGDACTVGTRPDMGMLSLGVSYRFQEDAAAPVVAAPAPAPEVATKH 212  
Db 61 EIAATRLEYCWNNTGDACTVGTRPDMGMLSLGVSYRFQEDAAAPVVAAPAPAPEVATKH 120  
Qy 213 FTLKSDVLNFENKATLKPGQQALDQLYTQLSNDPDKGSAAVVLGYTDIGSAYNOOL 272  
Db 121 FTLKSDVLNFENKATLKPGQQALDQLYTQLSNDPDKGSAAVVLGYTDIGSAYNOOL 180  
Qy 273 ERRAQSVDYLVAKGIPACKKISARGMGESENPTGNTCDNVKARAALIDCLAPDRRVEV 332  
Db 181 ERRAQSVDYLISKGIPADKISARGMGESENPTGNTCDNVKARAALIDCLAPDRRVEV 240  
Qy 333 KG 334  
Db 241 KG 242

Search completed: November 26, 2005, 00:10:29  
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